```
OM protein - protein search, using sw model

                                    GenCore version 5.1.6
                                    Copyright (c) 1993 - 2005 Compugen Ltd.

Run on:             December 24, 2005, 10:35:05 ; Search time 186 Seconds
                                    (without alignments)
                                    415.756 Million cell updates/sec

Title:              US-10-789-129-2
Perfect score:      910
Sequence:           1 MKASSLAFSLLSAAFYLLWT.........AVVKALGELDILIQWMEETE 176
Scoring table:      BLOSUM62
Searched:           Gapop 10.0 , Gapext 0.5
Searched:           2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters:       2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      A_Geneseq_21:*
                1:     geneseqp1980s:*
                2:     geneseqp1990s:*
                3:     geneseqp2000s:*
                4:     geneseqp2010s:*
                5:     geneseqp2002s:*
                6:     geneseqp2003as:*
                7:     geneseqp2003bs:*
                8:     geneseqp2004s:*
                9:     geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	910	100.0	176	2	AAY08661	Aay08661 Human Zcy
2	910	100.0	176	4	AAB85259	Aab85259 Human int
3	910	100.0	176	4	AAU04049	Aau04049 Human int
4	910	100.0	176	5	ABG67190	Abg67190 Inflammat
5	910	100.0	176	5	AAE29052	Aae29052 Human IL-
6	910	100.0	176	6	ABR62464	Abr62464 Human int
7	910	100.0	176	6	ABW00889	Abw00889 Human cyt
8	910	100.0	176	7	ADG46669	Adg46669 Human Zcy
9	910	100.0	176	8	ADJ83281	Adj83281 Human int
10	910	100.0	176	8	ADM95041	Adm95041 Human int
11	910	100.0	176	8	ADQ88067	Adq88067 Human Zcy
12	910	100.0	176	8	ADI16328	Adi16328 Human cyt
13	910	100.0	176	8	ADS18363	Ads18363 Human Zcy
14	910	100.0	176	9	ADV66904	Adv66904 Human IL-
15	910	100.0	176	9	ADW64518	Adw64518 Human IL-
16	910	100.0	176	9	ADX58772	Adx58772 Interleuk
17	910	100.0	176	9	AEA50049	Aea50049 Full leng
18	910	100.0	176	9	AEA28787	Aea28787 Human int
19	906	99.6	176	4	AAU12220	Aau12220 Human PRO
20	906	99.6	176	5	ABP52427	Abp52427 Human LP8
21	906	99.6	176	5	ABB82287	Abb82287 Human LP8
22	906	99.6	176	6	ABO17664	Abo17664 Novel hum
23	906	99.6	176	6	ABU80918	Abu80918 Human PRO
24	906	99.6	176	6	ABU66618	Abu66618 Human PRO
25	906	99.6	176	6	ABU59699	Abu59699 Novel sec
26	906	99.6	176	6	ABO24889	Abo24889 Human sec
27	906	99.6	176	6	ABU66894	Abu66894 Human sec
28	906	99.6	176	6	ADA45617	Ada45617 Novel hum
29	906	99.6	176	6	ADA76048	Ada76048 Human PRO
30	906	99.6	176	6	ADA18698	Ada18698 Homo sapi
31	906	99.6	176	6	ADA61321	Ada61321 Human PRO
32	906	99.6	176	6	ADB19106	Adb19106 Novel hum
33	906	99.6	176	6	ADB27647	Adb27647 Human PRO
34	906	99.6	176	6	ADA86126	Ada86126 Novel hum
35	906	99.6	176	6	ADB30278	Adb30278 Human PRO
36	906	99.6	176	6	ADA47476	Ada47476 Human PRO
37	906	99.6	176	6	ADB67271	Adb67271 Human PRO
38	906	99.6	176	6	ADB15690	Adb15690 Human hum
39	906	99.6	176	6	ADA85574	Ada85574 Novel hum
40	906	99.6	176	6	ADA96786	Ada96786 Human PRO
41	906	99.6	176	6	ADA79090	Ada79090 Human PRO
42	906	99.6	176	6	ADA87229	Ada87229 Human hum
43	906	99.6	176	6	ADB16431	Adb16431 Novel PRO
44	906	99.6	176	6	ADA91523	Ada91523 Novel hum
45	906	99.6	176	6	ADB14586	Adb14586 Human PRO

ALIGNMENTS

```
RESULT 1
AAY08661

ID     AAY08661 standard; protein; 176 AA.
XX
AC     AAY08661;
XX
DT     09-AUG-1999  (first entry)
XX
DE     Human Zcyto10 allele 1 protein.
XX
KW     Zcyto10; four alpha helix cytokine; vulnerary; cytostatic; haemostatic;
KW     anti-inflammatory; anti-asthmatic; growth factor; maintenance factor;
KW     trachea; salivary gland; stomach; pancreas; muscle; gene therapy; cancer;
KW     proliferation; differentiation; modulator; gastrointestinal tract;
KW     oral cavity; asthma; tracheobronchial tract; bronchitis; wound healing;
KW     platelet count; thrombocytopenia; human.
OS     Homo sapiens.
XX
PN     WO9927103-A1.
XX
PD     03-JUN-1999.
XX
PF     25-NOV-1998;  98WO-US025228.
XX
PR     26-NOV-1997;  97US-00979156.
XX
PA     (ZYMO ) ZYMOGENETICS INC.
XX
PI     Conklin DC, Haldeman BA, Grossmann A;
XX
DR     WPI; 1999-357840/30.
DR     N-PSDB; AAX77692.
XX
PT     New mammalian cytokine-like polynucleotide useful in the treatment of
PT     asthma and bronchitis.
XX
PS     Claim 1; Page 64-65; 82pp; English.
XX
CC     This invention describes a novel mammalian four alpha helix cytokine
CC     designated Zcyto10 which has vulnerary, cytostatic, anti-inflammatory,
CC     anti-asthmatic and haemostatic activity. Zcyto10 may be a growth and/or
CC     maintenance factor in the trachea and salivary glands, stomach, pancreas
CC     and muscle. Zcyto10 polynucleotides are useful as sources of primers and
CC     probes, and to determine if the Zcyto10 gene is present on chromosome 1,
CC     or to detect any mutations that may have occurred. Zcyto10
CC     polynucleotides are also useful as gene therapy reagents. The Zcyto10
```

```
CC  polypeptide, its fragments, and antibodies, as well as compounds
CC  identified as having binding affinity to Zcyto10, should be useful in the
CC  treatment of conditions associated with abnormal physiology or
CC  development, including conditions associated with abnormal proliferation, e.g. cancerous conditions,
CC  or degenerative conditions or altered immunity. The products are also
CC  useful for modulating cell proliferation, cell differentiation or
CC  cytokine production in the prevention or treatment of conditions
CC  characterized by abnormal cell proliferation, cell differentiation or
CC  cytokine production. Zcyto10 polypeptides, agonists and antagonists may
CC  be therapeutically useful in the regeneration of the gastrointestinal
CC  tract or oral cavity, as well as in the treatment of asthma, and other
CC  diseases of the tracheobronchial tract such as bronchitis. Zcyto10
CC  polypeptides may also be useful to promote wound healing, and to increase
CC  platelet count, e.g. in cancer patients who experience thrombocytopenia
CC  due to chemotherapy or radiation therapy
XX
SQ  Sequence 176 AA;
```

```
Query Match             100.0%;  Score 910;  DB 2;  Length 176;
Best Local Similarity   100.0%;  Pred. No. 5e-88;
Matches  176;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          1 MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSDIRGSVQAKDGNI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSDIRGSVQAKDGNI 60

Qy         61 DIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSFLTIK 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSFLTIK 120

Qy        121 KDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE 176
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE 176
```

```
RESULT 2
AAB85259
ID   AAB85259 standard; protein; 176 AA.
XX
AC   AAB85259;
XX
DT   07-SEP-2001  (first entry)
XX
DE   Human interleukin-20 (IL-20) receptor polypeptide.
XX
KW   Interleukin 20; IL-20; IL-20RA; ZcytoR7; IL-20RB; DIRS1; immunoglobulin;
KW   antiinflammatory; antipsoriatic; antiasthmatic; antibacterial;
KW   dermatological; antiulcer; antagonist.
XX
OS   Homo sapiens.
XX
PN   WO200146232-A2.
XX
PD   28-JUN-2001.
XX
PF   22-DEC-2000; 2000WO-US035307.
XX
PR   23-DEC-1999;  99US-00471774.
PR   22-JUN-2000; 2000US-0213416P.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Foster DC, Xu W, Madden KL, Kelly JD, Sprecher CA, Brandt CS;
PI   Rixon MW, Presnell SR, Fox BA;
XX
DR   WPI; 2001-398320/42.
XX
PT   Isolated interleukin 20 soluble receptor comprising two polypeptide
PT   subunits IL-20RA and IL-20RB, useful for down-regulating IL-20 and thus
PT   treating inflammatory diseases such as psoriasis.
XX
PS   Disclosure; Page 53-54; 119pp; English.
XX
```

```
CC  The invention relates to an interleukin 20 (IL-20) soluble receptor
CC  comprising two polypeptide subunits IL-20RA (formerly known as ZcytoR7)
CC  and IL-20RB (formerly known as DIRS1). The two subunits are preferably
CC  linked together. In one embodiment, one subunit is fused to the constant
CC  region of the light chain of an immunoglobulin, and the other subunit is
CC  fused to constant region of the heavy chain of an immunoglobulin. The
CC  light chain and the heavy chain are connected via a disulphide bond. The
CC  soluble receptor can be used to down-regulate IL-20 and thus treat
CC  inflammatory diseases such as psoriasis, inflammatory lung injury such as
CC  asthma or bronchitis, adult respiratory disease (ARD), septic shock,
CC  multiple organ failure, bacterial pneumonia, eczema, atopic and contact
CC  dermatitis, and inflammatory bowel disease such as ulcerative colitis and
CC  Crohn's disease. Sequences AaB85259-262 represent human IL-20 receptor
CC  polypeptide fragments
XX
SQ  Sequence 176 AA;
```

```
Query Match             100.0%;  Score 910;  DB 4;  Length 176;
Best Local Similarity   100.0%;  Pred. No. 5e-88;
Matches  176;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          1 MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSDIRGSVQAKDGNI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSDIRGSVQAKDGNI 60

Qy         61 DIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSFLTIK 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSFLTIK 120

Qy        121 KDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE 176
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE 176
```

```
RESULT 3
AAU04049
ID   AAU04049 standard; protein; 176 AA.
XX
AC   AAU04049;
XX
DT   23-OCT-2001  (first entry)
XX
DE   Human interleukin-20, IL-20, protein #1.
XX
KW   Human; interleukin-20; IL-20; antagonist; psoriasis; eczema; dermatitis;
KW   adult respiratory disease; asthma; bronchitis; pneumonia;
KW   multiple organ failure; inflammatory lung injury; septic shock;
KW   bacterial pneumonia; inflammatory bowel disease; rheumatoid arthritis;
KW   ulcerative colitis; Crohn's disease.
XX
OS   Homo sapiens.
XX
PN   WO200146261-A1.
XX
PD   28-JUN-2001.
XX
PF   22-DEC-2000; 2000WO-US035305.
XX
PR   23-DEC-1999;  99US-00470898.
PR   22-JUN-2000; 2000US-0213341P.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Thompson P, Foster DC, Wenfeng X, Madden KL, Kelly JD;
PI   Sprecher CA, Blumberg H, Eagan MA, Jaspers SR, Chandrasekher JA;
PI   Novak JE;
XX
DR   WPI; 2001-418045/44.
XX
PT   Treating interleukin-20 induced inflammation in a mammal, such as adult
PT   respiratory disease, eczema, psoriasis, contact dermatitis, multiple
PT   organ failure and septic shock, involves administering IL-20 antagonist.
XX
```

RESULT 4

```
ABG67190
ID   ABG67190 standard; protein; 176 AA.
XX
AC   ABG67190;
XX
DT   24-SEP-2002  (first entry)
XX
DE   Inflammatory disease related human interleukin (IL)20 polypeptide #1.
XX
KW   Inflammation; interleukin-20; IL-20; IL-8; chemokine;
KW   neutrophil; monocyte; basophil; eosinophil; chemoattractant; psoriasis;
KW   periodontal disease; rheumatoid arthritis; idiopathic pulmonary fibrosis;
KW   angiogenesis-dependent chronic inflammatory condition; lung cancer;
KW   melanoma; inflammatory disease; diabetes; arteriosclerosis; cataract;
KW   reperfusion injury; cancer; meningitis; rheumatic disease; skin disease;
KW   idiopathic pulmonary fibrosis; inflammatory bowel disease; psoriasis;
KW   ulcerative colitis; eczema; atopic dermatitis; contact dermatitis;
KW   inflammatory lung disease; ARD; adult respiratory disease; asthma;
KW   bronchitis; pneumonia.
XX
OS   Homo sapiens.
XX
PN   US2004042366-A1.
XX
PD   11-APR-2002.
XX
PF   22-DEC-2000; 2000US-0746359.
XX
PR   22-JUN-2000; 2000US-0213341P.
PR   23-DEC-1999; 99US-0171969P.
XX
PA   (THOM/) THOMPSON P.
PA   (FOST/) FOSTER D C.
PA   (XUWW/) XU W.
PA   (MADD/) MADDEN K L.
PA   (KELL/) KELLY J D.
PA   (SPRE/) SPRECHER C A.
PA   (BLUM/) BLUMBERG H.
PA   (EAGA/) EAGAN M A.
PA   (JASP/) JASPERS S R.
PA   (CHAN/) CHANDRASEKHER Y A.
PA   (NOVA/) NOVAK J E.
XX
PI   Thompson P,  Foster DC,   Xu W,  Madden KL,  Kelly JD,   Sprecher CA;
PI   Blumberg H,  Eagan MA,  Jaspers SR,  Chandrasekher YA,  Novak JE;
XX
DR   WPI; 2002-507215/54.
XX
PT   Treating inflammatory skin and lung diseases using antibodies against
PT   interleukins (IL)-20 (which indirectly modulates activation of IL-8),
PT   useful for treating e.g. psoriasis, asthma and bronchitis.
XX
PS   Claim 1; Page 47-48; 117pp; English.
XX
CC   The sequence is a Human interleukin-20, IL-20 protein of the invention.
CC   The invention relates to treating a mammal afflicted with a disease in
CC   which an interleukin-20 (IL-20) polypeptide plays a role, involves
CC   administering antagonist of IL-20 polypeptide to the individual. The
CC   method is useful for treating psoriasis, eczema, atopic dermatitis,
CC   contact dermatitis, adult respiratory disease, asthma, bronchitis and
CC   pneumonia and is also useful for treating multiple organ failure,
CC   inflammatory lung injury, septic shock, bacterial pneumonia, inflammatory
CC   bowel disease, rheumatoid arthritis, ulcerative colitis and Crohn's
CC   disease
XX
SQ   Sequence 176 AA;

        Query Match             100.0%;  Score 910;  DB 4;  Length 176;
        Best Local Similarity   100.0%;
        Matches  176;  Conservative    0;  Pred. No. 5e-88;
                       Mismatches   0;  Indels   0;   Gaps   0;

Qy          1 MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSSCVIATNLQEIRNGFSDIRGSVQAKDGNI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSSCVIATNLQEIRNGFSDIRGSVQAKDGNI 60

Qy         61 DIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSFLTIK 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSFLTIK 120

Qy        121 KDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE 176
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE 176
```

RESULT 5

```
AAE29052
ID   AAE29052 standard; protein; 176 AA.
XX
AC   AAE29052;
XX
DT   27-JAN-2003  (first entry)
XX
DE   Human IL-20 protein #1.
XX
KW   Human; heterodimeric cytokine receptor; interleukin-22R; IL-22R; asthma;
KW   inflammatory disease; psoriasis; adult respiratory disease; bronchitis;
KW   septic shock; multiple organ failure; inflammatory lung injury; eczema;
XX
PS   Claim 1; Page 12-13; 68pp; English.
XX
CC   The invention describes a method (I) for treating a mammal afflicted with
CC   a disease in which an interleukin-20 (IL-20) polypeptide plays a role
CC   comprising administering antagonist of the IL-20 polypeptide to the
CC   individual. An important cytokine in the inflammatory process is
CC   interleukin-8 (IL-8), a chemokine that acts as an agonist for neutrophils
CC   via chemotaxis and the release of granule enzymes. IL-8 binds to
CC   receptors on neutrophils, monocytes, basophils, and eosinophils. IL-8 is
CC   a potent chemoattractant for neutrophils; and the early stages of
CC   periodontal disease are characterized by the influx of neutrophils. IL-8
CC   is a potent inducer of angiogenesis in several angiogenesis-dependent
CC   chronic inflammatory conditions, including rheumatoid arthritis,
CC   psoriasis, and idiopathic pulmonary fibrosis. Additionally, IL-8 is an
CC   important source of angiogenic activity in human lung cancer. Also, IL-8
CC   expression correlates with experimental metastatic activity of some
CC   melanoma cell lines. Therefore an effective method to treat inflammatory
CC   diseases would be to administer an agent that would inhibit IL-8. It has
CC   been shown that IL-20 up-regulates IL-8. Therefore antagonists to IL-20
CC   can be used to treat these diseases. The method is used for treating
CC   diseases in which the IL-20 polypeptide plays a role e.g. inflammatory
CC   injury, cancer, meningitis, rheumatic bowel disease, idiopathic pulmonary
CC   fibrosis, inflammatory bowel disease, arteriosclerosis, cataracts, reperfusion
CC   (psoriasis, eczema, atopic dermatitis and contact dermatitis) or an
CC   inflammatory lung disease (adult respiratory disease (ARD), asthma,
CC   bronchitis and pneumonia). This sequence represents a human interleukin-
CC   20 (IL-20) polypeptide used in developing the method of the invention
XX
SQ   Sequence 176 AA;

        Query Match             100.0%;  Score 910;  DB 5;  Length 176;
        Best Local Similarity   100.0%;
        Matches  176;  Conservative    0;  Pred. No. 5e-88;
                       Mismatches   0;  Indels   0;   Gaps   0;

Qy          1 MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSSCVIATNLQEIRNGFSDIRGSVQAKDGNI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSSCVIATNLQEIRNGFSDIRGSVQAKDGNI 60

Qy         61 DIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSFLTIK 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSFLTIK 120

Qy        121 KDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE 176
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE 176
```

```
KW  bacterial pneumonia; dermatitis; ulcerative colitis; Crohn's disease;
KW  antiinflammatory; dermatological; antibacterial; immunosuppressive;
KW  antiulcer; ZcytoR11.
XX
OS  Homo sapiens.
XX
PN  WO20027260T-A2.
XX
PD  19-SEP-2002.
XX
PF  07-MAR-2002; 2002WO-US007214.
XX
PR  09-MAR-2001; 2001US-0274560P.
PR  21-JUN-2001; 2001US-0299865P.
XX
PA  (ZYMO ) ZYMOGENETICS INC.
XX
PI  Chandrasekher YA, Novak JE, Foster DC, Xu W, Jaspers SR;
XX
DR  WPI; 2002-723314/78.
XX
PT  Soluble heterodimeric cytokine receptor useful for down-regulating
PT  interleukin-20 and treating inflammatory diseases, such as psoriasis and
PT  asthma, comprises an interleukin-22R subunit and a interleukin-20RB
PT  subunit.
PS  Disclosure; Page 48; 82pp; English.
PT  The present invention relates to novel heterodimeric cytokine receptor
PT  which comprises an interleukin-22R (IL-22R; ZcytoR11)) subunit. Receptor
PT  sequences are useful for down-regulating IL-20 and treating inflammatory
CC  diseases such as psoriasis, inflammatory disease, multiple organ
CC  failure, septic shock, inflammatory lung injury such as bronchitis or
CC  asthma, bacterial pneumonia, eczema, atopic and contact dermatitis,
CC  ulcerative colitis and Crohn's disease. The present sequence is human
CC  interleukin-20 (IL-20) protein
XX
SQ  Sequence 176 AA;

Query Match             100.0%;  Score 910;  DB 5;  Length 176;
Best Local Similarity   100.0%;  Pred. No. 5e-88;
Matches 176;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSSCVIATNLQEIRNGFSDIRGSVQARDGNI 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSSCVIATNLQEIRNGFSDIRGSVQARDGNI 60

Qy          61 DIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSFLTIK 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 DIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSFLTIK 120

Qy         121 KDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE 176
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 KDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE 176

RESULT 6
ABR62464
ID  ABR62464 standard; protein; 176 AA.
XX
AC  ABR62464;
XX
DT  06-NOV-2003  (first entry)
XX
DE  Human interleukin-20.
XX
KW  Human; interleukin-20; IL-20; cervical cancer; cytostatic; virucide.
XX
OS  Homo sapiens.
XX
FH  Key             Location/Qualifiers
FT  Peptide         1. .24
FT                  /label= signal_peptide
```

```
FT  Protein         25. .176
FT                  /label= IL-20
XX
PN  WO2003051384-A1.
XX
PD  26-JUN-2003.
XX
PF  17-DEC-2002; 2002WO-US040309.
XX
PR  17-DEC-2001; 2001US-0341783P.
XX
PA  (LUNN/) LUNN P G.
XX
PI  Chandrasekher YA, McKernan PA;
XX
DR  WPI; 2003-569114/53.
DR  N-PSDB; ACF05161.
XX
PT  Inhibiting the growth and/or proliferation of cervical cancer cells,
PT  useful for treating cervical cancer or human papilloma virus infection,
PT  comprises bringing Interleukin-20 (IL-20) into contact with the cervical
PT  cancer cells.
PS  Disclosure; Page 12; 26pp; English.
CC  The present sequence is the protein sequence of human interleukin-20 (IL-
CC  20), including the signal sequence. The invention relates to the use of
CC  IL-20 for treating cervical cancer or cells infected with human papilloma
CC  virus. IL-20 can be administered alone or in conjunction with radiation
CC  or chemotherapeutic agents or surgical excision of the involved cells or
CC  lesions
XX
SQ  Sequence 176 AA;

Query Match             100.0%;  Score 910;  DB 6;  Length 176;
Best Local Similarity   100.0%;  Pred. No. 5e-88;
Matches 176;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSSCVIATNLQEIRNGFSDIRGSVQARDGNI 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSSCVIATNLQEIRNGFSDIRGSVQARDGNI 60

Qy          61 DIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSFLTIK 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 DIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSFLTIK 120

Qy         121 KDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE 176
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 KDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE 176

RESULT 7
ABW00889
ID  ABW00889 standard; protein; 176 AA.
XX
AC  ABW00889;
XX
DT  15-JAN-2004  (first entry)
XX
DE  Human cytokine-like polypeptide-10 (Zcyto10) #1.
XX
KW  Human; cytokine-like polypeptide-10; Zcyto10; therapy; thrombocytopaenia;
KW  autoimmune disease; insulin-dependent diabetes mellitus; immune response;
KW  rheumatoid arthritis; multiple sclerosis; infection; radiation therapy;
KW  asthma; bronchitis; wound healing; periodontal disease; antiinflammatory;
KW  psoriasis; eczema; dry skin; oral cavity; muscle atrophy; haemostatic;
KW  cancer; vulnerary.
XX
OS  Homo sapiens.
XX
FH  Key             Location/Qualifiers
FT  Peptide         1. .24
FT                  /label= signal_peptide
```

FT   Protein   25. .176
FT   /note= "Mature human Zcyto10"
FT   Disulfide-bond   33. .126
FT   Disulfide-bond   80. .132
FT   Disulfide-bond   81. .134
XX
PN   US657674 3-B1.
XX
DT   10-JUN-2003.
XX
PF   17-MAY-1999;   99US-00313458.
XX
PR   26-NOV-1997;   97US-0066597P.
PR   25-NOV-1998;   98US-00199586.
XX
PA   (ZYMO) ZYMOGENETICS INC.
XX
PI   Conklin DC, Haldeman BA;
XX
DR   WPI; 2003-799828/75.
DR   N-PSDB; AAD61821.
XX
PT   Claim 1; Col 31-32; 0pp; English.
XX
CC   Novel human cytokine-like polypeptide-10, Zcyto10, useful for treating
CC   insulin-dependent diabetes mellitus, rheumatoid arthritis, multiple
CC   sclerosis, asthma, psoriasis and inhibiting cancer cell growth.
PS
CC   The invention relates to an isolated human cytokine-like polypeptide-10
CC   (Zcyto10) polypeptide. Zcyto10 is useful for prevention or treatment of
CC   conditions characterised by improper cell proliferation, cell
CC   differentiation or cytokine production. Zcyto10 is useful for treating
CC   autoimmune diseases such as insulin-dependent diabetes mellitus,
CC   rheumatoid arthritis, multiple sclerosis, etc., by inhibiting cellular
CC   immune response. The invention is useful for inhibiting cancer cell
CC   growth or proliferation, for stimulating immune system to combat
CC   microbial or viral infections, for increasing platelet production, and
CC   thus useful in cancer patients who experience thrombocytopaenia due to
CC   cancer therapy or radiation therapy. Zcyto10 is useful in trachea-
CC   specific or tracheobronchial-specific applications, such as in the
CC   maintenance or would repair of the tracheobronchial epithelium or cells
CC   underlying the same, in regulating mucous production or mucociliary
CC   clearance of debris or in treatment of asthma, bronchitis or other
CC   diseases of the tracheobronchial tract. Zcyto10 may also enhance wound
CC   healing and promote regeneration of affected tissues which may be
CC   especially useful in the treatment of periodontal disease. Zcyto10 can be
CC   used to treat skin conditions such as psoriasis, eczema and dry skin in
CC   general. Zcyto10 is useful for regenerating gastrointestinal tract or
CC   oral cavity and for modulating muscle tone in the tracheobronchial tract,
CC   and for treating muscle atrophy in the elderly, sick or bed-ridden.
CC   Zcyto10 is also useful for promoting wound healing. The present sequence
CC   is human Zcyto10 protein
XX
SQ   Sequence 176 AA;

Query Match   100.0%; Score 910; DB 7; Length 176;
Best Local Similarity   100.0%;
Matches 176; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSDIRGSVQAKDGNI 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSDIRGSVQAKDGNI 60

Qy   61 DIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSFLTIK 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 DIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSFLTIK 120

Qy   121 KDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE 176
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 KDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE 176

RESULT 8

ADG46669
ID   ADG46669 standard; protein; 176 AA.
XX
AC   ADG46669;
XX
DT   11-MAR-2004 (first entry)
XX
DE   Human Zcyto10 protein #1.
XX
KW   cytokine-like polypeptide-10; Zcyto10; wound healing;
KW   platelet proliferation; wound repair; mucous production; asthma;
KW   bronchitis; tracheobronchial tract disease; periodontal disease;
KW   skin condition; psoriasis; eczema; dry skin; protein therapy; human;
KW   vulnerary; respiratory; antibronchitic; dental; dermatological.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   Peptide   1. .24
FT   /label= Signal-peptide
FT   Protein   25. .176
FT   /note= "Human mature Zcyto10 protein"
XX
PN   US2003176657-A1.
XX
PD   18-SEP-2003.
XX
PF   15-APR-2003; 2003US-00413661.
XX
PR   26-NOV-1997;   97US-0066597P.
PR   25-NOV-1998;   98US-00199586.
PR   17-MAY-1999;   99US-00313458.
XX
PA   (CONK/) CONKLIN D C.
PA   (HALD/) HALDEMAN B A.
XX
PI   Conklin DC, Haldeman BA;
XX
DR   WPI; 2003-863865/80.
DR   N-PSDB; ADG46668.
XX
PT   Claim 1; SEQ ID NO 2; 3lpp; English.
XX
CC   Novel isolated mammalian cytokine-like polypeptide-10 (Zcyto10), useful
CC   for treating asthma, bronchitis and other tracheobronchial damage.
PS
CC   The present invention relates to novel mammalian cytokine-like
CC   polypeptide-10 (Zcyto10) proteins and polynucleotides encoding such
CC   proteins. Sequences of the invention are useful for promoting the healing
CC   of wounds and for stimulating the proliferation of platelets. In
CC   particular Zcyto10 polypeptides may be used in trachea-specific or
CC   tracheobronchial-specific applications such as maintenance or wound
CC   repair of the tracheobronchial epithelium or cells underlying it; in
CC   regulating mucous production; mucociliary clearance of debris; in
CC   treatment of asthma, bronchitis and other diseases of the
CC   tracheobronchial tract. They are also used to promote regeneration of
CC   affected tissues which may be especially useful in the treatment of
CC   periodontal disease. Zcyto10 polypeptides can be used to treat skin
CC   conditions such as psoriasis, eczema and dry skin in general. They are
CC   also used in protein therapy. The present sequence is human Zcyto10
CC   protein.
XX
SQ   Sequence 176 AA;

Query Match   100.0%; Score 910; DB 7; Length 176;
Best Local Similarity   100.0%;
Matches 176; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSDIRGSVQAKDGNI 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSDIRGSVQAKDGNI 60

Qy   61 DIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSFLTIK 120

Left column

```
Db
Qy   121 KDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE 176
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 KDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE 176

Qy   61  DIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSPLTIK 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  DIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSPLTIK 120
```

RESULT 9

```
ID   ADJ83281 standard; protein; 176 AA.
XX
AC   ADJ83281;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Human interleukin IL-20 protein - SEQ ID 1.
XX
KW   inflammation; single chain antibody; interleukin; IL-20; IL-20RA subunit;
KW   IL-20RB subunit; antiinflammatory; dermatological; antipsoriatic;
KW   antiarthritic; respiratory; antiasthmatic; antiulcer; antibacterial;
KW   immunosuppressive; gastrointestinal; skin; psoriasis; eczema;
KW   atopic dermatitis; contact dermatitis; lung;
KW   adult respiratory distress syndrome; asthma; bronchitis; pneumonia;
KW   arthritis; septic shock; multiple organ failure; bowel;
KW   ulcerative colitis; Crohn's disease; human.
XX
OS   Homo sapiens.
XX
PN   US2004005320-A1.
XX
PD   08-JAN-2004.
XX
PF   28-APR-2003; 2003US-00424658.
XX
PR   23-DEC-1999;  99US-01719969P.
PR   22-JUN-2000;  2000US-02133419P.
PR   22-DEC-2000;  2000US-00746359.
XX
PA   (THOM/)  THOMPSON P.
PA   (FOST/)  FOSTER D C.
PA   (XUWW/)  XU W.
PA   (MADD/)  MADDEN K L.
PA   (KELL/)  KELLY J D.
PA   (SPRE/)  SPRECHER C A.
PA   (BLUM/)  BLUMBERG H.
PA   (EAGA/)  EAGAN M A.
PA   (JASP/)  JASPERS S R.
PA   (CHAN/)  CHANDRASEKHER Y A.
PA   (NOVA/)  NOVAK J E.
XX
PI   Thompson P, Foster DC, Xu W, Madden KU, Kelly JD, Sprecher CA;
PI   Blumberg H, Eagan MA, Jaspers SR, Chandrasekher YA, Novak JE;
XX
DR   WPI; 2004-081696/08.
XX
```

Disclosure; SEQ ID NO 1; 69pp; English.

Reducing or treating inflammation, e.g. inflammatory lung disease,
comprises administering an antibody, antibody fragment or single chain
antibody that specifically binds to an interleukin (IL)-20 receptor of
an IL-20 receptor.

The invention relates to a novel method of reducing or treating
inflammation in a mammal which comprises administering an antibody,
antibody or single chain antibody which specifically binds to a
receptor of interleukin (IL)-20 comprising an IL-20RA subunit and an IL-
20RB subunit. The method of the invention has antiinflammatory,
dermatological, antipsoriatic, antiarthritic, respiratory, antiasthmatic,
antiulcer, antibacterial, immunosuppressive and gastrointestinal
applications and may be useful for reducing or treating an inflammation,
including an inflammatory skin disease such as psoriasis, eczema, atopic
dermatitis and contact dermatitis or an inflammatory lung disease such as

Right column

```
CC   adult respiratory distress syndrome, asthma, bronchitis and pneumonia, as
CC   well as arthritis, septic shock, multiple organ failure, inflammatory
CC   bowel disease, ulcerative colitis or Crohn's disease. The current
CC   sequence is that of the human IL-20 protein of the invention.
XX
SQ   Sequence 176 AA;

Query Match             100.0%;  Score 910;  DB 8;  Length 176;
Best Local Similarity   100.0%;  Pred. No. 5e-88;
Matches  176;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   61  DIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSPLTIK 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  DIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSPLTIK 120

Qy   121 KDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE 176
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 KDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE 176
```

RESULT 10

```
ID   ADM95041 standard; protein; 176 AA.
XX
AC   ADM95041;
XX
DT   17-JUN-2004  (first entry)
XX
DE   Human Interleukin-20 (IL-20) protein SeqID3.
XX
KW   colon cancer; interleukin 20 receptor alpha chain;
KW   IL-20 receptor alpha chain; cytostatic; human.
XX
OS   Homo sapiens.
XX
PN   JP2004075569-A.
XX
PD   11-MAR-2004.
XX
PF   12-AUG-2002; 2002JP-00234880.
XX
PR   12-AUG-2002; 2002JP-00234880.
XX
PA   (TAKE )  TAKEDA CHEM IND LTD.
XX
DR   WPI; 2004-320878/30.
DR   N-PSDB; ADM95042.
XX
PT   Agent useful for prevention and/or treatment of colon cancer, comprises
PT   interleukin 20 (IL-20), IL-20 receptor alpha chain, IL-20 receptor beta
PT   chain.
XX
PS   Disclosure; SEQ ID NO 9; 50pp; Japanese.
```

This invention relates to a novel agent for prevention and/or treatment
of colon cancer, comprising of the interleukin 20 (IL-20) receptor alpha
chain, its partial peptide or salt. The invention may be useful for the
development of compounds with a cytostatic activity. The invention is
useful for preventing and/or treating colon cancer. A diagnostic agent is
useful for diagnosis of colon cancer. By using IL-20, IL-20 receptor, its
salt or its peptide, compounds that have altered binding property towards
them can be efficiently screened. The present sequence is that of the
human Interleukin-20 protein which is related to the invention.

```
XX
SQ   Sequence 176 AA;

Query Match             100.0%;  Score 910;  DB 8;  Length 176;
Best Local Similarity   100.0%;  Pred. No. 5e-88;
Matches  176;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   1   MKASSLLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSDIRGSVQAKDGNI 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1   MKASSLLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSDIRGSVQAKDGNI 60
```

RESULT 11

```
ID   ADQ88067 standard; protein; 176 AA.
AC   ADQ88067;
DT   07-OCT-2004  (first entry)
DE   Human Zcyto10 longer form protein.
```

```
KW   Mammalian cytokine-like polypeptide-10; Zcyto10; cell proliferation;
KW   cell differentiation; cytokine production; autoimmune disease;
KW   insulin dependent diabetes mellitus; multiple sclerosis;
KW   rheumatoid arthritis; cancer; wound healing; tissue regeneration;
KW   platelet count; asthma; skin disease; psoriasis; eczema; dry skin;
KW   antidiabetic; neuroprotective; antirheumatic; antiarthritic; cytostatic;
KW   immunostimulant; vulnerary; antiasthmatic; antipsoriatic; dermatological;
KW   gene therapy; human.
OS   Homo sapiens.
```

```
FH   Key             Location/Qualifiers
FT   Peptide         1..24
FT                   /label= Signal_peptide
FT   Protein         25..176
FT                   /note= "Human mature Zcyto10 protein"
FT   Disulfide-bond  33..126
FT                   /note = Intramolecular disulfide bond
FT   Disulfide-bond  80..132
FT                   /note = Intramolecular disulfide bond
FT   Disulfide-bond  81..134
FT                   /note = Intramolecular disulfide bond
```

```
PN   US200412428-A1.
PD   22-JUL-2004.
PF   27-FEB-2004; 2004US-00789129.
PR   26-NOV-1997;  97US-0066597P.
PR   25-NOV-1998;  98US-0019958G.
PR   15-APR-2003;  2003US-00413661.
PA   (ZYMO ) ZYMOGENETICS INC.
PI   Conklin DC, Haldeman BA;
DR   WPI; 2004-5525564/53.
DR   N-PSDB; ADQ88066.
```

```
PT   New Zcyto10 polypeptides and polynucleotides, useful for treating
PT   autoimmune diseases (e.g. insulin dependent diabetes mellitus, multiple
PT   sclerosis or rheumatoid arthritis), or skin conditions (e.g. psoriasis or
PT   eczema]
PS   Claim 1; SEQ ID NO 2; 31pp; English.
CC   The present invention provides mammalian cytokine-like polypeptide-10
CC   (Zcyto10) proteins and their encoding polynucleotides. The invention is
```

```
Qy   1    MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSDIRGSVQAKDGNI  60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1    MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSDIRGSVQAKDGNI  60

Qy   61   DIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSFLTIK  120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61   DIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSFLTIK  120

Qy   121  KDLRLJCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE  176
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  KDLRLJCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE  176
```

RESULT 12

```
ID   ADR16328 standard; protein; 176 AA.
AC   ADR16328;
DT   21-OCT-2004  (first entry)
DE   Human cytokine-like polypeptide-10 (Zcyto10) long form protein.
```

```
KW   Cytokine-like polypeptide-10; Zcyto10; therapy; asthma; infection;
KW   psoriasis; eczema; dry skin; wound healing; platelet proliferation;
KW   human.
OS   Homo sapiens.
```

```
FH   Key             Location/Qualifiers
FT   Peptide         1..24
FT                   /label= Signal_peptide
FT   Protein         25..176
FT                   /note= "Mature Zcyto10 long form protein"
FT   Disulfide-bond  33..126
FT   Disulfide-bond  80..132
FT   Disulfide-bond  81..134
```

```
PN   US200415287B-A1.
PD   05-AUG-2004.
PF   27-FEB-2004; 2004US-00789968.
PR   26-NOV-1997;  97US-0066597P.
PR   25-NOV-1998;  98US-0019958G.
PR   15-APR-2003;  2003US-00413661.
PA   (ZYMO ) ZYMOGENETICS INC.
PI   Conklin DC, Haldeman BA;
DR   WPI; 2004-580197/56.
DR   N-PSDB; ADR16327.
```

```
CC   useful for treating conditions characterised by improper cell
CC   proliferation, cell differentiation or cytokine production, specifically
CC   for treating autoimmune diseases such as insulin dependent diabetes
CC   mellitus, multiple sclerosis and rheumatoid arthritis and for inhibiting
CC   cancer cell growth. The invention is also used to stimulate the immune
CC   system, to enhance wound healing and promote regeneration of affected
CC   tissues, to increase platelet count and to treat asthma and skin
CC   conditions such as psoriasis, eczema and dry skin. The invention acts as
CC   an antidiabetic, neuroprotective, antirheumatic, antiarthritic,
CC   cytostatic, immunostimulant, vulnerary, antiasthmatic, antipsoriatic and
CC   dermatological agent. The invention is also used in gene therapy. The
CC   present sequence is human Zcyto10 longer form protein.
```

```
SQ   Sequence 176 AA;

Query Match     100.0%;  Score 910;  DB 8;  Length 176;
Best Local Similarity  100.0%;
Matches 176;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
```

```
Qy   1    MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSDIRGSVQAKDGNI  60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1    MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSDIRGSVQAKDGNI  60

Qy   61   DIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSFLTIK  120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61   DIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSFLTIK  120

Qy   121  KDLRLJCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE  176
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  KDLRLJCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE  176
```

RESULT 13

```
ADS18363
ID   ADS18363 standard; protein; 176 AA.
XX
AC   ADS18363;
XX
DT   02-DEC-2004  (first entry)
XX
DE   Human Zcyto10 protein #1.
XX
KW   Zcyto10; cytokine-like polypeptide; cell proliferation;
KW   cell differentiation; autoimmune disease; diabetes; multiple sclerosis;
KW   rheumatoid arthritis; asthma; psoriasis; cancer; wound; gene therapy;
KW   immunosuppressive; antidiabetic; neuroprotective; antirheumatic;
KW   antiarthritic; antiasthmatic; antipsoriatic; cytostatic; vulnerary;
KW   human.
XX
OS   Homo sapiens.
XX
FH   Key              Location/Qualifiers
FT   Peptide          1..24
FT                    /label= Signal_peptide
FT   Protein          25..176
FT                    /note= "Mature Zcyto10 protein"
FT   Disulfide-bond   33..126
FT   Region           35
FT                    /note= "Helix A"
FT   Region           49
FT                    /note= "Helix A"
FT   Region           91
FT                    /note= "Helix B"
FT   Region           105
FT                    /note= "Helix B"
FT   Region           112
FT                    /note= "Helix B"
FT   Region           126
FT                    /note= "Helix C"
FT   Region           158
FT                    /note= "Helix C"
FT   Region           172
FT                    /note= "Helix D"
FT                    /note= "Helix D"
XX
PN   US2004181040-A1.
XX
PD   16-SEP-2004.
XX
PF   29-DEC-2003; 2003US-00748484.
XX
PR   26-NOV-1997;   97US-0066597P.
PR   25-NOV-1998;   98US-00199586.
PR   15-APR-2003; 2003US-00413661.
XX
PA   (CONK/) CONKLIN D C.
PA   (HALD/) HALDEMAN B A.
PA   (GROS/) GROSSMANN A.
XX
PI   Conklin DC, Haldeman BA, Grossmann A;
XX
DR   WPI; 2004-667683/65.
DR   N-PSDB; ADS18362.
XX
PT   New isolated antibody that binds to a Zcyto10 polypeptide, useful for
PT   treating asthma, microbial or viral infections, and for promoting the
PT   healing of wounds, psoriasis, eczema or dry skin.
XX
PS   Claim 1; SEQ ID NO 2; 32pp; English.
XX
CC   The invention relates to novel cytokine-like polypeptide (Zcyto10)
CC   polypeptides and polynucleotides. Zcyto10 sequences are useful for
CC   treating asthma, microbial or viral infections, psoriasis, eczema or dry
CC   skin, for promoting the healing of wounds and for stimulating the
CC   proliferation of platelets. The present sequence is human Zcyto10
CC   protein.
XX
SQ   Sequence 176 AA;

  Query Match             100.0%;  Score 910;  DB 8;  Length 176;
  Best Local Similarity   100.0%;  Pred. No. 5e-88;
  Matches 176;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1  MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSDIRGSVQAKDGNI 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSDIRGSVQAKDGNI 60

Qy   61  DIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSFLTIK 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  DIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSFLTIK 120

Qy  121  KDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE 176
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  KDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE 176
```

RESULT 14

```
ADV66904
ID   ADV66904 standard; protein; 176 AA.
XX
AC   ADV66904;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Human IL-20 wild-type, SEQ ID 20.
XX
KW   Dermatological; Antiinflammatory; Interleukin-20 antagonist;
KW   interleukin-20; IL-20; cytokine; dermatological disease; inflammation.
XX
OS   Homo sapiens.
XX
PN   US2004248097-A1.
XX
PT   New antibody that selectively binds to a Zcyto10 polypeptide useful for
PT   modulating cell proliferation, cell differentiation or cytokine
PT   production in the prevention or treatment of e.g. autoimmune diseases,
PT   cancer or wounds.
XX
PS   Claim 1; SEQ ID NO 2; 31pp; English.
XX
CC   The present invention relates to a mammalian cytokine-like polypeptide,
CC   Zcyto10 and its encoding polynucleotide. The invention is useful for
CC   modulating cell proliferation, cell differentiation or cytokine
CC   production in the prevention or treatment of conditions such as
CC   autoimmune diseases (e.g. diabetes, multiple sclerosis, rheumatoid
CC   arthritis, asthma or psoriasis) and cancer or wounds. The invention is
CC   also useful in gene therapy. The present sequence is the human Zcyto10
CC   protein.
XX
SQ   Sequence 176 AA;

  Query Match             100.0%;  Score 910;  DB 8;  Length 176;
  Best Local Similarity   100.0%;  Pred. No. 5e-88;
  Matches 176;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1  MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSDIRGSVQAKDGNI 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSDIRGSVQAKDGNI 60

Qy   61  DIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSFLTIK 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  DIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSFLTIK 120

Qy  121  KDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE 176
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  KDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE 176
```

PD   09-DEC-2004.
XX
PF   23-MAY-2003; 2003US-0044765.
PR   23-MAY-2003; 2003US-0044765.
XX
PA   (CHAN/) CHANG M.
XX
PI   Chang M;
XX
DR   WPI; 2005-072805/08.
XX
PS   Disclosure; SEQ ID NO 20; 27pp; English.
XX
PT   keratinocyte growth factor-1 or reactive oxygen species in a cell.
PT   increasing the level of interleukin-6, tumor necrosis factor-alpha,
PT   New interleukin-20 alternatively spliced polypeptides, useful for
XX
CC   The present invention relates to alternatively spliced interleukin (IL)-
CC   20 variants (I; ADV66885 and ADV66901). IL-20 is a member of the IL-
CC   ADV66887-ADV66901). IL-20 is a member of the IL-10 family of cytokines.
CC   Members in this family are important in controlling inflammation
CC   responses. (I) is useful for increasing the level of IL-6, Tumor Necrosis
CC   Factor (TNF)-alpha, Keratinocyte Growth Factor-1 (KGF-1) or reactive
CC   oxygen species in a cell, which involves contacting (I) with a cell. (II)
CC   is useful for identifying a compound for treating an IL-20-induced
CC   disease, which involves contacting a compound with a cell containing a
CC   nucleic acid comprising IL-20 promoter operably linked to a reporter
CC   gene, and determining the expression level of the reporter gene in the
CC   cell, where the expression level of the reporter gene in the absence of
CC   the compound, if lower than that in the presence of the compound,
CC   indicates that the compound is a candidate for treating IL-20 induced
CC   disease. The IL-20-induced disease is a skin disease or an inflammatory
CC   disease. The present sequence is the wild-type human IL-20 sequence,
CC   which was used in an alignment with the alternatively spliced human IL-20
CC   variant sequence.
XX
SQ   Sequence 176 AA;

Query Match   100.0%; Score 910; DB 9; Length 176;
Best Local Similarity   100.0%;
Matches 176; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSDIRGSVQAKDGNI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSDIRGSVQAKDGNI 60

Qy   61 DIRILRRTESLQDTKPANRCCLLRHLLRIYLDRVFKNYQTPDHYTLRKISSLANSFLTIK 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 DIRILRRTESLQDTKPANRCCLLRHLLRIYLDRVFKNYQTPDHYTLRKISSLANSFLTIK 120

Qy   121 KDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE 176
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 KDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE 176

RESULT 15
ADW64518
ID   ADW64518 standard; protein; 176 AA.
XX
AC   ADW64518;
XX
DT   24-MAR-2005 (first entry)
XX
DE   Human IL-20 protein, seqid:1.
XX
KW   Therapy; cns-gen.; respiratory-gen.; antiasthmatic; antipsoriatic;
KW   antiinflammatory; psoriasis; dermatological disease; immune disorder;
KW   pulmonary disease; asthma; inflammation; respiratory disease; bronchitis;
KW   antiinflammatory; inflammation; cystic fibrosis;
KW   gastrointestinal disease; chemotherapy; interleukin.
XX
OS   Homo sapiens.

XX
PN   US2005003475-A1.
XX
PD   06-JAN-2005.
XX
PD   22-DEC-2000; 2000US-00745792.
XX
PF   22-DEC-2000; 2000US-00745792.
XX
PR   23-DEC-1999; 99US-0171966P.
PR   22-JUN-2000; 2000US-0213416P.
XX
PA   (FOST/) FOSTER D C.
PA   (XUWW/) XU W.
PA   (MADD/) MADDEN K L.
PA   (KELL/) KELLY J D.
PA   (SPRE/) SPRECHER C A.
PA   (BRAN/) BRANDT C S.
PA   (RIXO/) RIXON M W.
PA   (PRES/) PRESNELL S R.
PA   (FOXB/) FOX B A.
XX
PI   Foster DC, Xu W, Madden KL, Kelly JD, Sprecher CA, Brandt CS;
PI   Rixon MW, Presnell SR, Fox BA;
XX
DR   WPI; 2005-065240/07.
XX
PT   New isolated soluble receptor comprised of an interleukin 20 receptor
PT   alpha (IL-20Rα) subunit and a IL-20RB subunit, useful for treating
PT   inflammatory diseases e.g., psoriasis and inflammatory lung diseases
PT   e.g., asthma.
XX
PS   Disclosure; SEQ ID NO 1; 73pp; English.
XX
CC   The present invention relates to an soluble receptor having an
CC   interleukin 20 receptor alpha (IL-20Rα) subunit and an IL-20RB subunit.
CC   The invention is useful for treating inflammatory diseases such as
CC   psoriasis and inflammatory lung diseases such as asthma, bronchitis and
CC   cystic fibrosis. The present sequence is the human IL-20 protein.
XX
SQ   Sequence 176 AA;

Query Match   100.0%; Score 910; DB 9; Length 176;
Best Local Similarity   100.0%;
Matches 176; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSDIRGSVQAKDGNI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSDIRGSVQAKDGNI 60

Qy   61 DIRILRRTESLQDTKPANRCCLLRHLLRIYLDRVFKNYQTPDHYTLRKISSLANSFLTIK 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 DIRILRRTESLQDTKPANRCCLLRHLLRIYLDRVFKNYQTPDHYTLRKISSLANSFLTIK 120

Qy   121 KDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE 176
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 KDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE 176

Search completed: December 24, 2005, 10:42:59
Job time : 187 secs

This Page Blank (uspto)

OM protein - protein search, using sw model

Copyright (c) 1993 - 2005 Compugen Ltd.

GenCore version 5.1.6

Run on: December 24, 2005, 10:39:36 ; Search time 38 Seconds
(without alignments)
445.636 Million cell updates/sec

Title: US-10-789-129-2
Perfect score: 910
Sequence: 1 MKASSLAFSLLSAAFVLLWT........AVVKALGELIDLLQWMEETE 176

Scoring table: BLOSUM62
              Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : PIR_80:*
            1: pir1:*
            2: pir2:*
            3: pir3:*
            4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	156.5	17.2	178	2	A38580	interleukin-10 pre
2	155	17.0	170	1	Q0BE2	BCRP1 protein - hu
3	155	17.0	175	2	I46591	interleukin 10 - P
4	147.5	16.2	179	2	A48558	interleukin 10 hom
5	144	15.8	178	2	A34853	interleukin-10 pre
6	136	14.9	178	2	JN0475	interleukin-10 pre
7	94.5	10.4	567	2	JC5538	Rab geranylgeranyl
8	94.5	10.4	567	2	A45977	Rab geranylgeranyl
9	93.5	10.3	809	2	S64594	Rab geranylgeranyl
10	85	9.3	140	2	F83128	probable beta-adap
11	81.5	9.0	646	2	T33366	hypothetical prote
12	81	8.9	1062	2	S46367	hypothetical prote
13	80	8.8	542	2	T19925	protein kinase CDC
14	76.5	8.4	502	2	AD3160	hypothetical prote
15	76.5	8.4	553	2	B90153	2-isopropylmalate
16	76	8.4	523	2	S64826	probable membrane
17	76	8.4	917	2	T21870	hypothetical prote
18	75	8.2	276	2	B71517	probable synchococ
19	75	8.2	726	2	T48023	ATP-dependent RNA
20	75	8.2	729	2	T21870	probable pre-mRNA
21	74.5	8.2	121	2	E83640	hypothetical prote
22	74.5	8.2	1047	2	D71302	probable exonuclea
23	74	8.1	682	1	H69879	ATP-dependent DNA
24	73.5	8.1	449	2	B71917	udp-n-acetylmurama
25	73.5	8.1	653	2	D87602	sensory box histid
26	73.5	8.1	729	2	F97321	membrane export pr
27	73.5	8.1	782	2	S33945	late protein, 100K
28	73.5	8.1	794	2	A98211	hypothetical prote
29	73.5	8.1	794	2	C86057	hypothetical prote
30	73	8.0	471	2	B38637	Ras inhibitor (clo
31	73	8.0	563	2	D90531	exoinuclease ABC s
32	73	8.0	614	2	E83880	hypothetical prote
33	73	8.0	1008	2	D84434	probable receptor-
34	72.5	8.0	261	2	H98213	transcription repr
35	72.5	8.0	388	2	T00641	hypothetical prote
36	72.5	8.0	409	2	A54750	TNF receptor assoc
37	72.5	8.0	447	2	T20552	hypothetical prote
38	72.5	8.0	481	2	S39682	ywbL protein - Bac
39	72.5	8.0	1101	2	T33153	ywbL protein - Bac
40	72.5	8.0	2182	2	T28634	variant-specific s
41	72.5	8.0	2581	2	AF2545	hypothetical prote
42	72	7.9	255	2	F81833	hypothetical prote
43	72	7.9	255	2	E81197	hypothetical prote
44	72	7.9	279	2	A70081	conserved hypothet
45	72	7.9	351	2	S74651	conserved hypothet

ALIGNMENTS

RESULT 1
A38580
interleukin-10 precursor - human
interleukin-10 precursor - human (CSIF); IL-10
interleukin-10 precursor - human; cytokine synthesis inhibitory factor
N;Alternate names: cytokine synthesis inhibitory factor (CSIF); IL-10
C;Species: Homo sapiens (man)
C;Date: 14-Feb-1992 #sequence revision 14-Feb-1992 #text_change 09-Jul-2004
C;Accession: A38580; G01539; S49110; 137890
A;Residues: 1-178 <SAN>
A;Cross-references: UNIPARC:UPI000000034E50; EMBL:U16720; NID:g1041812; PIDN:AAA80104.1;
R;Kube, D.; Platzer, C.; von Knethen, A.; Straub, H.; Hafner, M.; Tesch, H.
Proc. Natl. Acad. Sci. U.S.A. 88, 1172-1176, 1991
submitted to the EMBL Data Library, March 1994
A;Accession: 137890
A;Description: Isolation of the human interleukin-10-promoter. Characterization of the
A;Reference number: S49110
R;Sanjanwala, B.
submitted to the EMBL Data Library, October 1994
A;Reference number: G07695
A;Accession: G01539
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-178 <SAN>
A;Cross-references: UNIPARC:UPI00000178477; EMBL:X78437; NID:g1167482
R;Platzer, C.; Volk, H.D.; Platzer, M.
DNA Seq. 4, 399-401, 1994
A;Title: 5' noncoding sequence of human IL-10 gene obtained by oligo-cassette PCR walk
A;Reference number: 137890; MUID:95143580; PMID:7841162
A;Accession: 137890
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-6 <PLA>
A;Cross-references: UNIPARC:UPI00001EB9; EMBL:X73536; NID:g452395; PIDN:CAA51942.1;
C;Genetics:
A;Gene: GDB:IL10; IL-10
A;Cross-references: GDB:128636; OMIM:124092
A;Map position: 1q31-1q32
A;Introns: 55/3; 75/3; 126/3; 148/3
C;Superfamily: interleukin-10

C;Keywords: cytokine; glycoprotein; lymphokine; T-cell
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-178/Product: interleukin-10 #status predicted <MAT>
F;30-126,80-132/Disulfide bonds: #status experimental
F;134/Binding site: carbohydrate (Asn) (covalent) #status predicted

```
Query Match      17.2%;  Score 156.5; DB 2; Length 178;
Best Local Similarity   27.4%;  Pred. No. 8.1e-08;
Matches   43;  Conservative   32;  Mismatches   71;  Indels   11;  Gaps   5;

Qy   22 STGLKTLNLGSCV-----IATNLQEIRNGFSDIRGSVQAKDGNIDIRILRRTESLQDTKP 76
                      ::| :||||| ::|||| | |||::||| :
Db   19 SPGQGTQSENSCTHFPGNLPNMLRDLRDAFSRVKTFFQMKD-QLD-NLLKESLLEDFKG 76

Qy   77 ANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSFLTIKDLRLCHAHMTCHCGE 136
              :::| |                         ||    |||    |||||
Db   77 YLGCQALSEMIQFYLEEVMPQAENQDPDIKAHVNSLGENLKTLRLRLRRCHRFLPC---E 133

Qy  137 EAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWME 173
              |:  :| |||||||||||| |||        :
Db  134 NKSKAVEQVKNAFNKLQ-EKGIYKAMSEFDIFINYIE 169
```

RESULT 2
QQBE2
BCRF1 protein - human herpesvirus 4 (strain B95-8)
C;Species: human herpesvirus 4, Epstein-Barr virus
C;Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 09-Jul-2004
R;Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.
Mol. Biol. Med. 1, 21-45, 1983
A;Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr viru
A;Reference number: A93065; MUID:85035713; PMID:6092825
A;Accession: A03741
A;Molecule type: DNA
A;Residues: 1-170 <BAN>
A;Cross-references: UNIPROT:P03180; UNIPARC:UPI0000000CDBE; EMBL:V01555; NID:G59074; PIDN
R;Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.; H
Nature 310, 207-211, 1984
A;Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.
A;Reference number: A03794; MUID:84270667; PMID:6087149
A;Contents: annotation; protein coding region
C;Superfamily: interleukin-10

```
Query Match      17.0%;  Score 155; DB 1; Length 170;
Best Local Similarity   28.9%;  Pred. No. 1.1e-07;
Matches   39;  Conservative   29;  Mismatches   61;  Indels   6;  Gaps   4;

Qy   39 LQEIRNGFSDIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNY 98
                                                         :::| |
Db   34 LRDLRDAFSRVKTFFQTKD-EVD-NLLKESLLEDFKGYLGCQALSEMIQFYLEEVMPQA 91

Qy   99 QTPDHYTLRKISSLANSFLTIKDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAV 158
                                 ||    |||    |||||     |:  :| |||||||||
Db   92 ENQDPEAKDHVNSLGENLKTLRLRLRRCHRFLPC---ENKSKAVEQIKNAFNKLQ-EKGI 147

Qy  159 VKALGELDILLQWME 173
        |||        :
Db  148 YKAMSEFDIFINYIE 162
```

RESULT 3
I46591
interleukin 10 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C;Accession: I46591
R;Blancho, G.; Gianello, P.; Germana, S.; Baetscher, M.; Sachs, D.H.; LeGuern, C.
Proc. Natl. Acad. Sci. U.S.A. 92, 2800-2804, 1995
A;Title: Molecular identification of porcine interleukin 10: regulation of expression in
A;Reference number: I46591; MUID:95224028; PMID:7708727
A;Accession: I46591
A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA
A;Residues: 1-175 <BLA>
A;Cross-references: UNIPROT:Q29055; UNIPARC:UPI000012D476; GB:L20001; NID:g309792; PIDN:
C;Genetics:
A;Gene: Il-10
C;Superfamily: interleukin-10

```
Query Match      17.0%;  Score 155; DB 2; Length 175;
Best Local Similarity   27.0%;  Pred. No. 1.1e-07;
Matches   48;  Conservative   34;  Mismatches   78;  Indels   18;  Gaps   6;

Qy  116 FLTIKDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWME 173
              ||    |||    |||||     |:  :| |||||||||| |||        :
Db  112 LKTLRLRLRRCHQFLPC---ENKSKAVEVKSAFSKLQ-ERGVYKAMGEFDIFINYIE 165
```

RESULT 4
A48558
interleukin 10 homolog - equine herpesvirus 2
N;Alternate names: hypothetical protein E7
C;Species: equine herpesvirus 2
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C;Accession: A48558; S55664
R;Rode, H.J.; Janssen, W.; Rosen-Wolff, A.; Bugert, J.J.; Thein, P.; Becker, Y.; Darai,
Virus Genes 7, 111-116, 1993
A;Title: The genome of equine herpesvirus type 2 harbors an interleukin 10 (IL10)-like g
A;Reference number: A48558; MUID:93227565; PMID:8385838
A;Accession: A48558
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-179 <ROD>
A;Cross-references: UNIPROT:Q89451; UNIPARC:UPI000012D058; GB:U20824; NID:g695172; PIDN
A;Note: Sequence extracted from NCBI backbone (NCBIN:129334, NCBIP:129335)
R;Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J. Mol. Biol. 249, 520-528, 1995
A;Title: The DNA sequence of equine herpesvirus 2.
A;Reference number: S55594; MUID:95302501; PMID:7783207
A;Accession: S55664
A;Status: preliminary; nucleic acid sequence not shown; translation not shown

```
Query Match      16.2%;  Score 147.5; DB 2; Length 179;
Best Local Similarity   31.9%;  Pred. No. 6.1e-07;
Matches   44;  Conservative   24;  Mismatches   59;  Indels   11;  Gaps   6;

Qy    1 MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCV-----IATNLQEIRNGFSDIRGSVQA 55
                                                            :::| |
Db    1 MPSSALLYCLI-----FLAGVAASIKSEN--SCIHFPTSLPHMLRELRAAFGPVKSFFQT 53

Qy   56 KDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANS 115
                                                                       ||
Db   54 KDQMGD--LILTGSLLEDFKGYLGCQALSEMIQFYLEDVMPKAESDGEDIKEHVNSLGEK 111

Qy  116 FLTIKDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWME 173
              ||    |||    |||||     |:  :| |||||||||| |||        :
Db  112 LKTLRLRLRRCHQFLPC---ENKSKAVEEVKSAFSKLQ-ERGVYKAMGEFDIFINYIE 165
```

```
Qy   39 QTPDHYTLR--KISSLANSFLTIKDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQ 155
                                  ||    |||    |||||     |:  :| ||||||
Db   41 LHELRAAFSRVKTFFQMKD-QLD-NMLLDGSLLEDFKGYLGCQALSEMIQFYLEEVMP-- 96

Qy  156 AAVVKALGELDILLQWME 173
        |||        :
Db   97 QAENHSTDQEKDKVNSLGEKLKTLRVRLRRCHRFLPC--ENKSKAVEQVKSAFSKLQ-E 152

Qy  153 KGVYKAMSEFDIFINYIE 170
```

RESULT 5
A34853
interleukin-10 precursor - mouse

N;Alternate names: cytokine synthesis inhibitory factor (CSIF); IL-10
C;Species: Mus musculus (house mouse)
A;Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 09-Jul-2004
A;Accession: A34853; I56136
A;Cross-references: UNIPROT:P18893; UNIPARC:UPI000002149B;
R;Moore, K.W.; Vieira, P.; Fiorentino, D.F.; Trounstine, M.L.; Khan, T.A.; Mosmann, T.R.
Science 248, 1230-1234, 1990
A;Accession: I56136
A;Title: Homology of cytokine synthesis inhibitory factor (IL-10) to the Epstein-Barr vi
R;Reference number: A34853; MUID:90273182; PMID:2161559
A;Accession: A34853
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-178 <MOO>
A;Cross-references: UNIPROT:P18893; UNIPARC:UPI000002149B; GB:M37897; NID:g198280; PIDN:
R;Kim, J.M.; Brannan, C.I.; Copeland, N.G.; Jenkins, N.A.; Khan, T.A.; Moore, K.W.
J. Immunol. 148, 3618-3623, 1992
A;Title: Structure of the mouse IL-10 gene and chromosomal localization of the mouse and
A;Reference number: I56136; MUID:92268508; PMID:1350294
A;Accession: I56136
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-178 <RES>
A;Cross-references: UNIPARC:UPI000002149E; GB:M84340; NID:g198291; PIDN:AAA39275.1; PID:
C;Genetics:
A;Gene: IL10
A;Introns: 55/3; 75/3; 126/3; 148/3
C;Superfamily: cytokine; lymphokine; T-cell

Query Match 15.8%; Score 144; DB 2; Length 178;
Best Local Similarity 31.1%; Pred. No. 1.3e-06;
Matches 42; Conservative 19; Mismatches 68; Indels 6; Gaps 4;

```
Qy  39 LQEIRNGFPSDIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNY  98
Db  41 LLELRTAFSQVKTFFQTKD-QLD-NILLTDSLMQDFKGYLGCQALSEMIQFYLVEVMPQA   98

Qy  99 QTPDHYTLRKISSLANSFLTIKKDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAV  158
Db  99 EKHGPEIKEHLNSLGEKLKTLRMRLRRCHRFLPC---ENKSKAVEQVKSDFNKLQDQ-GV  154

Qy 159 VKALGELDILLQWME 173
Db 155 YKAMNEFDIFINCIE 169
```

RESULT 6
JN0475
N;Alternate names: cytokine synthesis inhibitory factor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JN0475; JC1357; S36021
R;Feng, L.; Tang, W.W.; Chang, J.C.; Wilson, C.B.
Biochem. Biophys. Res. Commun. 192, 452-458, 1992
A;Title: Molecular cloning of rat cytokine synthesis inhibitory factor (IL-10) cDNA and
A;Reference number: JN0475
A;Accession: JN0475
A;Molecule type: nucleic acid sequence not shown
A;Residues: 1-178 <FEN>
A;Cross-references: UNIPROT:P29456; UNIPARC:UPI000167959
R;Goodman, R.E.; Oblak, J.; Bell, R.G.
Biochem. Biophys. Res. Commun. 189, 1-7, 1992
A;Title: Synthesis and characterization of rat interleukin-10 (IL-10) cDNA clones from t
A;Reference number: JC1357; MUID:93080542; PMID:1280414
A;Accession: JC1357
A;Molecule type: mRNA
A;Residues: 1,'P',3-64,'L',66-178 <GOO>
A;Cross-references: UNIPARC:UPI000120477; GB:L02926; NID:g204903; PIDN:AAA41425.1; PID:
R;Feng, L.
submitted to the EMBL Data Library, July 1991
A;Reference number: S36021
A;Accession: S36021

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-178 <FE2>
A;Cross-references: UNIPARC:UPI000167959; EMBL:X60675; NID:g296620; PIDN:CAA43090.1;
A;Superfamily: interleukin-10
C;Cross-references: UNIPARC:UPI000167959;
C;Superfamily: interleukin-10
C;Keywords: cytokine; glycoprotein; lymphokine; T-cell
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-178/Product: interleukin-10 #status predicted <MAT>
F;29,134/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.9%; Score 136; DB 2; Length 178;
Best Local Similarity 28.5%; Pred. No. 8e-06;
Matches 53; Conservative 26; Mismatches 77; Indels 30; Gaps 8;

```
Qy   1 MKASSLAFSLLSAAFYLLWTPSTGLKKTNLGSCVIATN--------------------LQEIRNGFPSD 48
Db   1 MLGSALLCLLLLA----------------GVKT-SKSHSIRGDNNCTHFPVSQTHMLRELRAAFSQ    50

Qy  49 IRGSVQAKDGNIDIRILRRTES-LQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLR 107
Db  51 VKTFFQKKD-QLDNIVL--TDSLLQDFKGYLGCQALSEMIKFYLVEVMPQAENHGPEIKE 107

Qy 108 KISSLANSFLTIKKDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDI 167
Db 108 HLNSLGEKLKTLWIQLRRCHRFLPC---ENKSKAVEQVKDFNKLQDK-GVYKAMNEFDI  163

Qy 168 LLQWME 173
Db 164 FINCIE 169
```

RESULT 7
JC5538
N;Rab geranylgeranyl transferase
C;Species: Homo sapiens (man)
C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 09-Jul-2004
C;Accession: JC5538
R;Song, H.J.; Rossi, A.; Ceci, R.; Kim, I.G.; Anzano, M.A.; Jang, S.I.; De Laurenzi, V
Biochem. Biophys. Res. Commun. 235, 10-14, 1997
A;Title: The genes encoding geranylgeranyl transferase alpha-subunit and transglutamin
A;Reference number: JC5538; MUID:97339427; PMID:9196026
A;Accession: JC5538
A;Molecule type: DNA
A;Residues: 1-567 <SON>
A;Cross-references: UNIPROT:Q92696; UNIPARC:UPI00001318BE
C;Comment: This protein is involved in cutaneous disease. The gene of this enzyme is p
A;Gene: Rabggta
A;Genetics:
A;Introns: 1/3; 38/3; 81/1; 143/1; 211/1; 238/2; 278/3; 300/3; 336/2; 354/2; 383/2; 41

Query Match 10.4%; Score 94.5; DB 2; Length 567;
Best Local Similarity 25.8%; Pred. No. 0.35;
Matches 49; Conservative 26; Mismatches 82; Indels 33; Gaps 9;

```
Qy   1 MKASSLAFSLLSAAFYLLWTPSTGLKKTNLGSCVIATNLQE--IRNGFSD---IRGSVQA 55
Db 304 LPAASLNDQLPQHTFPRVIWTAGDVQK-----ECVLLKGRQBGWCRDSTTDEQLRCELSV 358

Qy  56 KDGNIDIRILRRTESLQDTKPANRCCLLRHLL-------RLYLDRVFKNYQT----PDH 103
Db 359 EKSTVLQSELESCKELQELEPENKWCLLTILLMRALDPLLYEKRTLQYFQTLKAVDPMR 418

Qy 104 YT----LRKISSLANSFLTIK----KDLRLCHAHMTCHCGEEAMKKYSQI-LSH--FEKL 152
Db 419 ATYLDLRSKFLLENSVLKMEYAEVRVLHLAHKDLTVLCHLEQLLLVTHLDLSHNRLRTL 478

Qy 153 EPQAAVVKAL 162
Db 479 PPALAALRCL 488
```

RESULT 8

A45977
Rab geranylgeranyl transferase component B alpha subunit - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A45977
R;Armstrong, S.A.; Seabra, M.C.; Sudhof, T.C.; Goldstein, J.L.; Brown, M.S.
J. Biol. Chem. 268, 12221-12229, 1993
A;Title: cDNA cloning and expression of the alpha and beta subunits of rat Rab geranylge
A;Reference number: A45977; MUID:93282201; PMID:8505342
A;Accession: A45977
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 1-567 <ARM>
A;Cross-references: UNIPROT:Q08602; UNIPARC:UPI0000131B8F; GB:S62096; NID:g385474; PIDN:
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIN:133369, NCBIP:133370)

Query Match   10.4%; Score 94.5; DB 2; Length 567;
Best Local Similarity   24.2%; Pred. No. 0.35;
Matches 46; Conservative 31; Mismatches 80; Indels 33; Gaps 8;

Qy   1 MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQE--IRNGFSD--IRGSVQA 55
           | :|| : :: |:| :: : :|: |:| || |:| ||:|: ||:|::
Db   304 LPAASLNDQLPQHTFRVIWTGSDSQK------ECVLLKDRPECWCRDSATDEQLFRCELSV 358

Qy   56 KDGNIDIRILRRTESLQDTKPANRCCLLRHLLRL-YLDRVFKNYQTPDHYT-------- 105
             ::||| |:| || | ||:| | : | |::|: |||:|:|:|:||:||
Db   359 EKSTVLQSELBSCKELQELEPENKWCLLTIILLMRALDPLLYEKETLQYFSTLKAVDPMR 418

Qy   106 -----LRKISSLANSFLTIK------KDLRLCHAHMTCHCGEEAMKKYSQI-LSH--FEKL 152
                 | :||| |:|:| |: |||| || ||| ||:| |:| ||:|
Db   419 AAYLDDLRSKFLLENSVLKMEYADVRVLHLAHKDLTVLCHLEQLLLVTHDLLSHNRLRAL 478

Qy   153 EPQAAVVKAL 162
           | |:| |:|
Db   479 PPALAALRCL 488

RESULT 9
S64594
probable beta-adaptin YKS5 - Yeast (Saccharomyces cerevisiae)
N;Alternate names: protein G9331; protein YGR261c
C;Species: Saccharomyces cerevisiae
C;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 09-Jul-2004
C;Accession: S64594; S63450
R;Panzeri, L.; Agostoni Carbone, M.L.; Melchioretto, P.; Plevani, P.; Martegani, E.; Van
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64591
A;Accession: S64594
A;Molecule type: DNA
A;Residues: 1-809 <PAN>
A;Cross-references: UNIPROT:P46682; UNIPARC:UPI00000530A8; EMBL:Z73046; NID:g1323474; PI
A;Experimental source: strain S288C
R;Robinson, L.C.; Engle, H.M.; Panek, H.R.
submitted to the EMBL Data Library, September 1995
A;Description: Suppressors of loss of yeast casein kinase 1 function define the four sub
A;Reference number: S63439
A;Accession: S63450
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-26, 'PLSWVNPP', 36-723, 'T', 725-795, 801-809 <ROB>
A;Cross-references: UNIPROT:P46682; EMBL:U35411; NID:g1017728; PID:g1017729
A;Gene: SGD:YKS5
A;Genetics: SGD:S003493; MIPS:YGR261c
A;Map position: 7R

Query Match   10.3%; Score 93.5; DB 2; Length 809;
Best Local Similarity   24.1%; Pred. No. 0.66;
Matches 48; Conservative 39; Mismatches 73; Indels 39; Gaps 10;

Qy   2 KASSLLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSDIRGSVQAKDGNID 61
           ||:::| || :: ||:| :||::| :|:|: : :| :| : |::||:|:| ||: :|
Db   21 EAAAVATSKLGESSYTYY---SQNINPQQLVTLLNSRNSREVRDAMKRIISIMASDDDSID 78

RESULT 10
F83128
probable transcription regulator PA4135 [imported] - Pseudomonas aeruginosa (strain PA01
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: F83128
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathc
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: F83128
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-140 <STO>
A;Cross-references: UNIPROT:Q9HWP6; UNIPARC:UPI000000C5C2C; GB:AE004830; GB:AE004091; NIC
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA4135

Query Match   9.3%;   Score 85; DB 2; Length 140;
Best Local Similarity   24.5%; Pred. No. 0.56;
Matches 25; Conservative 25; Mismatches 42; Indels 10; Gaps 3;

Qy   62 IRI----LRRTESLQDTKPANRCCLLRHLLIRLYLDRVFKNYQTPDHYTLRKISSLANSFL 117
           ||| || | | ||:|||| | | :| | :|:|:| |||||||||:|::| ||||||
Db   79 VQLYFADVVKNITTNDTK---------VKRLIHYLLRFAEN---DPNLTLLSINSLQKSLS 128

Qy   118 TIKDLRLCHAHMTCHCGEEAMKKYSQILSHFEK----LEPQA------AVVK-ALGE 164
           || |:| :||| | |:|: | ||:: | | |:|:| |:| |:||
Db   129 DSNSELR-CPA--LSALSDMKMSSLAPIILHTVKKLVTDPSAMVRGEVALAIIKLYRAGK 185

Qy   165 ------LDILLQWMEETE 176
                  | ::| | || |
Db   186 NDYHEELLDILKELMADTD 204

RESULT 11
T33346
hypothetical protein C16A11.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33346
R;Johnson, D.; Biewald, T.
submitted to the EMBL Data Library, July 1998
A;Description: The sequence of C. elegans cosmid C16A11.
A;Reference number: Z21128
A;Accession: T33346
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-646 <JOH>
A;Cross-references: UNIPROT:O76579; UNIPARC:UPI000000765551; EMBL:AF077536; PIDN:AAC26261
A;Experimental source: strain Bristol N2; clone C16A11
C;Genetic:
A;Gene: CESP:C16A11.5
A;Genetic:
A;Map position: 2
A;Introns: 35/3; 72/1; 94/3; 129/3; 184/3; 205/1; 279/3; 387/3; 505/2; 540/2; 570/3

Query Match   9.0%;   Score 81.5; DB 2; Length 646;
Best Local Similarity   26.1%; Pred. No. 7.5;
Matches 36; Conservative 22; Mismatches 49; Indels 31; Gaps 8;

Qy   116 ---FLITIKDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEP 154
               | | |:| :|||| | |:|: | ||:: | | |
Db   40 IRILRQQGEMESYQLANQACILRPSMTGVLARLERDGIVRRWKAPKDQR-RVYVNLTEKG 98

Qy   99 QQCFVSMSGDMEKNYQRIQERFGEEKLAQLLELLNELKKIKP 140

A;Molecule type: DNA
A;Residues: 1-542 <WIL>
A;Cross-references: UNIPROT:Q18616; UNIPARC:UPI00001788837; EMBL:Z69787; PIDN:CAA93638.
A;Experimental source: clone C44C10
A;Genetics:
A;Gene: CESP:C44C10.4
A;Map position: X
A;Introns: 66/3; 229/3; 309/1; 328/3; 398/3

Query Match   8.8%; Score 80; DB 2; Length 542;
Best Local Similarity 23.2%; Pred. No. 8.5;
Matches   29; Conservative 25; Mismatches 43; Indels 28; Gaps 4;

Qy   29 NLGSCVIATNLQEIRNGFSDIRGSVQAKDGNIDIRILR-------RTESLQDTKPANRC 80
Db   176 NQGACFVDRSLEQ-RNSNGDHLPIVQELDSMKSIEFIQHPIQRAKHKAVPIEDLKPGSYC 234

Qy   81 CL-LRHLLRLYLD-----RVFKNYQTPD--HYTLRKISSLANSFLTIKKDLRLCHAHMTC 132
Db   235 ILAVDALFELFNEIIWGSRVFEKHKVPKIIBYVL-KIPT----LLFKSELRPHFIKTA 288

Qy   133 HCGEBAMKKYSQILSHFE 150
Db   289 H------LHRLIASFE 298

RESULT 12
S46367
protein kinase CDC7 (EC 2.7.1.-) - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
A;Cross-references: UNIPROT:P41892; UNIPARC:UPI0000127259; EMBL:X78799; NID:g521098; PID
A;Experimental source: wildtype 972 h minus
A;Note: mRNA sequencing was also done to confirm the intron borders
submitted to the EMBL Data Library, February 1999
R;Saunders, D.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
A;Reference number: 221860
A;Accession: T39888
R;Fankhauser, C.; Simanis, V.
EMBO J. 13, 3011-3019, 1994
A;Title: The cdc7 protein kinase is a dosage dependent regulator of septum formation in
A;Reference number: S46367; MUID:94313982; PMID:8034497
A;Accession: S46367
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1062 <SAU>
A;Cross-references: UNIPARC:UPI0000127259; EMBL:AL035537; PIDN:CAB36886.1; GSPDB:GN00067
A;Experimental source: strain 972h-; cosmid c21
A;Genetics:
A;Gene: CDC7; SPDB:SPBC21.06c
A;Map position: II; 2
A;Introns: 9/3; 54/3; 64/3; 86/2; 171/1; 325/1; 405/3; 427/1; 544/3; 589/3
A;Description: essential for septum formation and cell division
F;Function:
A;Keywords: ATP; cell division; phosphotransferase; protein kinase
F;7-259/Domain: protein kinase homology <KIN>
F;15-23/Region: protein kinase ATP-binding motif

Query Match   8.9%; Score 81; DB 2; Length 1062;
Best Local Similarity 30.2%; Pred. No. 15;
Matches   32; Conservative 20; Mismatches 44; Indels 10; Gaps 4;

Qy   23 TGLKTLNLGSCVIATNLQEIRNG-FSDIRGSVQAKDGNIDIRILRRTESLQDTKPANRCC 81
Db   466 TGLGTLVLANKCYGSWNNENEDGEESDIFDSIETNLENLDIE----NNIALDKRTHLAS 520

Qy   82 LLRHLRLYLDRVFKNYQTPDHYTLRKISSLANSFLTIKKDLRLCH 127
Db   521 LLSSLLGSLRD---KNIGSKD-TTVSQISAILSBDLSLKREIIQAH 562

RESULT 13
T19925
hypothetical protein C44C10.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
R;Cottage, A.
submitted to the EMBL Data Library, February 1996
A;Reference number: Z19197
A;Accession: T19925
A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA
A;Residues: 1-542 <FAN>
A;Cross-references: UNIPROT:UPI000012725; EMBL:AL035537; PIDN:CAB36886.1; GSPDB:GN00067
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 05-Oct-2004
A;Gene: CDC7; T39888
A;Accession: S46367; T39888
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 05-Oct-2004
A;Status: nucleic acid sequence not shown

RESULT 14
AD3160
hypothetical protein glnP/glnQ [imported] - Agrobacterium tumefaciens (strain C58, Dup
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
A;Accession: AD3160
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Woo,
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McCle
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Molecule type: DNA
A;Residues: 1-502 <KUR>
A;Cross-references: UNIPROT:Q9WWF4; UNIPARC:UPI00000D146D; GB:AE008687; PIDN:AAL45698.1
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: glnP/glnQ
A;Genome: plasmid

Query Match   8.4%; Score 76.5; DB 2; Length 502;
Best Local Similarity 24.6%; Pred. No. 17;
Matches   42; Conservative 23; Mismatches 37; Indels 69; Gaps 10;

Qy   39 LQEIRNGFSDIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNY 98
Db   212 IQETKEKFVAEQLKVNAKANAKMPLRISRVSEAIPKQTPSPN----------FKNN 256

Qy   99 ------QTPDHY----TLRKISSLANSFLTIKKDL---RLCHAHNTCHCGEEAMKKYSQI 145
Db   257 AIVVRPKTHNHYDNLITVDKLNSYLNEKVTERRELLQFAVNHPNMNIRFSEEGPNIYARE 316

Qy   146 LSHFE 150
Db   317 IDYTE 321

RESULT 15
B90153
2-isopropylmalate synthase, probable (leuA-1) [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
A;Accession: B90153

Query Match   8.4%; Score 76.5; DB 2; Length 502;
Best Local Similarity 24.6%; Pred. No. 17;
Matches   42; Conservative 23; Mismatches 37; Indels 69; Gaps 10;

Qy   10 LISAAFYLLWT-PSTGL------KTLNLGS---CVIATNLQEIRNGFSDIRGSVQA----- 55
Db   206 LLAGVFYLITVPLTHVNAIDRRLRIGKQRPSVITSGLEBV----SELDGAARASGVAF 261

Qy   56 KDGNIDIRILRRTESLQD------TKPANRCC---------LLRHL-------- 86
Db   262 KGGSLDVRLGMAYGDLDVLKGVDLSVKPGSVTCIIGFSGSGKSTLLRGINRLVEPKSGD 321

Qy   87 ------------LRLYLDRVFKNYQT-PDHYTLRKISSLANSFLTIKK 121
Db   322 ILIDGESILAMKPETLRRRVGMVFQHFNLFPDH------TALENVMLSLKK 366

R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.;
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: B90153
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-553 <KUR>
A;Cross-references: UNIPROT:Q98OZ1; UNIPARC:UPI000006418D; GB:AB006641; NID:g13813259; P
C;Genetics:
A;Gene: leuA-1
C;Superfamily: 2-isopropylmalate synthase leuA

Query Match   8.4%;   Score 76.5;   DB 2;   Length 553;
Best Local Similarity 19.6%;   Pred. No. 19;
Matches 39;   Conservative 34;   Mismatches 61;   Indels 65;   Gaps 8;

```
Qy    24  GLKTLNLGSCVIATNLQEIRNGFSDIRGSVQA---------------KDGNID-----------IRILRR  67
              |:|: : ||| :  :|: :|::    |:|:: ||                    ||            |    ||
Db   232  GIHAHNDIGCAVANSLMAIKAGARHVQGTINGIGERTGNADLIQIIPTLILKMGLNALNG  291

Qy    68  TESLQDTKPANRCC-----------------------------LLRHLLRLYLDRVFKNYQTPDH-------  103
              ||| : :|                                  :||:|  ::  || | :|
Db   292  QESLRKLREVSRIVTBILGLPPNPYQPYVGDNAPAHKAGVHVDAVMKVPRAYEHVDPSLV  351

Qy   104  ------YTLRKISSLAN--SFL-------TIKKDLRLCHAHMTCHCGEEAMKKYSQILSHFE  150
                      : ||  :  |  :|           ::|::  :::
Db   352  GNDRKFVISELSGTANLVSYLQGLGIAVDKDERL------------KKALNKIKELEARGY  401

Qy   151  KLE--PQAAVVKALGELDI  167
              ||:  |:||  |:|:|
Db   402  SFDVGPASAILITLKELNI  420
```

Search completed: December 24, 2005, 10:48:30
Job time : 39 secs

OM protein - protein search, using sw model

Copyright (c) 1993 - 2005 Compugen Ltd.

GenCore version 5.1.6

Run on: December 24, 2005, 10:35:50 ; Search time 230 Seconds
(without alignments)
539.883 Million cell updates/sec

Title: US-10-789-129-2
Perfect score: 910
Sequence: 1 MKASSLLAFSLLSAAFYLLWT.............AVVKALGELDLILQWMEETE 176

Scoring table: BLOSUM62
Gapop 10:0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	906	99.6	176	1	IL20_HUMAN	Q9NYY1 homo sapien
2	672	73.8	176	1	IL20_MOUSE	Q9JKv9 mus musculu
3	337.5	37.1	176	1	IL19_HUMAN	Q9UHd0 homo sapien
4	337.5	37.1	177	1	Q5VUT3_HUMAN	Q5VUT3 homo sapien
5	306	33.6	168	2	Q4LDR4_BRARE	Q4LDR4 brachydanio
6	281.5	30.9	176	1	IL19_MOUSE	Q8c170 mus musculu
7	266.5	29.3	175	2	Q7Sx60_TETNG	Q7Sx60 tetraodon n
8	222	24.4	220	2	Q92553_MOUSE	Q92553 mus musculu
9	220	24.2	181	2	Q92554_MOUSE	Q92554 mus musculu
10	217	23.8	206	2	IL24_HUMAN	Q13007 homo sapien
11	217	23.8	207	2	Q53X27_HUMAN	Q53x27 homo sapien
12	191	21.0	183	2	MOB5_RAT	Q9I124 rattus norv
13	187	20.5	183	2	Q9WVP8_RAT	Q9WVP8 rattus norv
14	175.5	19.3	175	2	Q6A2H5_CHICK	Q6a2h5 gallus gall
15	175.5	19.3	175	2	Q6A2H4_CHICK	Q6a2h4 gallus gall
16	161.5	17.7	178	1	IL10_MACNE	P51497 macaca neme
17	161	17.7	177	2	Q8UZJ6_9GAMA	Q8UZJ6 cercopithec
18	157.5	17.3	178	1	IL10_MACFA	P79338 macaca fasc
19	157.5	17.3	178	1	IL10_MACMU	P51496 macaca mula
20	157.5	17.3	178	1	IL10_PAPHA	Q5qov6 papio hamad
21	157.5	17.3	160	2	Q7T3I1_CYPCA	Q7t3i1 cyprinus ca
22	156.5	17.2	178	2	Q71UZ1_HUMAN	Q71uz1 homo sapien
23	156.5	17.2	178	1	IL10_FELCA	P55029 felis silve
24	156.5	17.2	178	1	IL10_HUMAN	P22301 homo sapien
25	156.5	17.2	178	2	Q6FGW4_HUMAN	Q6fgw4 homo sapien
26	155	17.0	170	1	IL10H_EBV	P03180 epstein-bar
27	155	17.0	170	2	Q77H2_9GAMA	Q77h2 human herpe
28	155	17.0	175	1	IL10_PIG	Q20055 sus scrofa
29	154.5	17.0	178	1	IL10_CERTO	P46651 cercocebus
30	153	16.8	178	1	IL10_MERUN	P47965 meriones un
31	151.5	16.6	179	1	IL10_CEREL	P51746 cervus elap
32	151	16.6	178	1	IL10_RABIT	Q9tsj4 oryctolagus
33	147.5	16.2	178	2	Q9TVD3_RABIT	Q9tvd3 oryctolagus
34	147.5	16.2	179	1	IL10H_EHV2	P68678 equine herp
35	147.5	16.2	179	1	IL10H_EHV2T	P68677 equine herp
36	147	16.2	178	1	IL10_MOUSE	P18893 mus musculu
37	145.5	16.0	178	2	Q6FGS9_HUMAN	Q6fgs9 homo sapien
38	144.5	15.9	160	2	Q923T1_SIGHI	Q923t1 sigmodon hi
39	144.5	15.9	174	1	IL10_TRIVU	Q97798 trichosurus
40	144.5	15.9	178	1	IL10_HORSE	Q28374 equus cabal
41	143.5	15.8	178	2	Q6VV71_BUBBU	Q6vv71 bubalus bub
42	143	15.7	178	2	Q90SL1_CHV12	Q90sl1 cercopithec
43	142.5	15.7	171	1	IL10_BOVIN	P43480 bos taurus
44	142.5	15.7	178	2	Q8MKG9_SAISC	Q8mkg9 saimiri sci
45	142	15.6	181	1	IL10_CANPA	P48411 canis famil

RESULT 1
IL20_HUMAN

ID IL20_HUMAN   STANDARD;   PRT;   176 AA.
AC Q9NYY1; Q96QZ6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Interleukin-20 precursor (IL-20) (Four alpha helix cytokine Zcyto10).
GN Name=IL20; Synonyms=ZCYTO10; ORFNames=UNQ852/PRO1801;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21097717; PubMed=11163236; DOI=10.1016/S0092-8674(01)00187-8;
RA Blumberg H., Conklin D., Xu W.F., Grossmann A., Brender T.,
RA Carollo S., Eagan M., Foster D., Haldeman B.A., Hammond A., Haugen H.,
RA Jelinek L., Kelly J.D., Madden K., Maurer M.F., Parrish-Novak J.,
RA Prunkard D., Sexson S., Sprecher C., Waggie K., West J.,
RA Whitmore T.E., Yao L., Kuechle M.K., Dale B.A., Chandrasekher Y.A.;
RT "Interleukin 20: discovery, receptor identification, and role in
RT epidermal function.";
RL Cell 104:9-19(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA Nickerson D.A.;
RT "SeattleSNPs, NHLBI HL66682 program for genomic applications, UW-
RT FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,
RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=22382257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

ALIGNMENTS

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP PROTEIN SEQUENCE OF 25-39.
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Henzel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites.";
RL Protein Sci. 13:2819-2824(2004).

-!- FUNCTION: Cytokine that may be involved in epidermal function and
-!- psoriasis. Acts through STAT3.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed at very low levels in skin, trachea,
-!- and other tissues.
-!- SIMILARITY: Belongs to the IL-10 family.

DR EMBL; AF224266; AAF36679.1; -; mRNA.
DR EMBL; AF402002; AAK84423.1; -; Genomic_DNA.
DR EMBL; AY358320; AAQ88686.1; -; mRNA.
DR EMBL; BC069311; AAH69311.1; -; mRNA.
DR EMBL; BC069364; AAH69364.1; -; mRNA.
DR EMBL; BC069398; AAH69398.1; -; mRNA.
DR EMBL; BC069425; AAH69425.1; -; mRNA.
DR EMBL; BC069449; AAH69449.1; -; mRNA.
DR EMBL; BC069487; AAH69487.1; -; mRNA.
DR EMBL; BC069523; AAH69523.1; -; mRNA.
DR EMBL; BC069559; AAH69559.1; -; mRNA.
DR EMBL; BC074948; AAH74948.1; -; mRNA.
DR EMBL; BC074949; AAH74949.1; -; mRNA.
DR HSSP; Q9UHD0; 1N1F.
DR Ensembl; ENSG00000162891; Homo sapiens.
DR HGNC; HGNC:6002; IL20.
DR MIM; 605619; -.
DR InterPro; IPR012351; Cytokine 4 hlx.
DR InterPro; IPR013352; IL-10_add_helix.
DR InterPro; IPR000098; Interleukin_10.
DR Pfam; PF00726; IL10; 1.
DR ProDom; PD003687; Interleukin_10; 1.
DR PROSITE; PS00520; INTERLEUKIN_10; 1.
DR GO; GO:0005576; C:extracellular region; TAS.
DR GO; GO:0005615; F:interleukin-20 receptor binding; TAS.
DR GO; GO:0030097; P:hemopoiesis; ISS.
DR GO; GO:0045606; P:positive regulation of epidermal cell diffe...; TAS.
DR GO; GO:0045618; P:positive regulation of keratinocyte differe...; TAS.
DR GO; GO:0042517; P:positive regulation of tyrosine phosphoryla...; TAS.
DR GO; GO:0050727; P:regulation of inflammatory response; TAS.
KW Cytokine; Direct protein sequencing; Signal.
FT SIGNAL 1 24
FT CHAIN 25 176 Interleukin-20.
FT DISULFID 33 126 Potential.
FT DISULFID 80 132 Potential.
FT DISULFID 81 134 Potential.

FT CONFLICT 48 48 E -> D (in Ref. 1).
FT CONFLICT 126 126 C -> S (in Ref. 3).
SQ SEQUENCE 176 AA; 20072 MW; 838599250B6C447 CRC64;

Query Match 99.6%; Score 906; DB 1; Length 176;
Best Local Similarity 99.4%; Pred. No. 1.8e-80;
Matches 175; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSDRGSVQAKDGNI 60
     ||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db 1 MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSDRGSVQAKDGNI 60

Qy 61 DIRILRRTESLLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSFLTIK 120
      ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db 61 DIRILRRTESLLQDTKPANRCCLLRHLLRLYLDRVEKNYQTPDHYTLRKISSLANSFLTIK 120

Qy 121 KDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE 176
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 KDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE 176

RESULT 2
ID IL20_MOUSE STANDARD; PRT; 176 AA.
AC Q9JKV9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Interleukin-20 precursor (IL-20) (Four alpha helix cytokine ZCYTO10).
GN Name=Il20; Synonyms=Zcyto10;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin;

RX MEDLINE=21097717; PubMed=11163236; DOI=10.1016/S0092-8674(01)00187-8;
RA Blumberg H., Conklin D., Xu W.F., Grossmann A., Brender T.,
RA Carollo S., Eagan M., Foster D., Haldeman B.A., Hammond A., Haugen H.,
RA Jelinek L., Kelly J.D., Madden K., Maurer M.F., Parrish-Novak J.,
RA Prunkard D., Sexson S., Sprecher C., Waggie K., West J.,
RA Whitmore T.E., Yao L., Kuechle M.K., Dale B.A., Chandrasekher Y.A.;
RT "Interleukin 20: discovery, receptor identification, and role in
RT epidermal function.";
RL Cell 104:9-19(2001).

-!- FUNCTION: Cytokine that may be involved in epidermal function and
-!- psoriasis. Acts through STAT3.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the IL-10 family.

DR EMBL; AF224267; AAF36680.1; -; mRNA.
DR HSSP; Q9UHD0; 1N1F.
DR Ensembl; ENSMUSG00000026416; Mus musculus.
DR MGI; MGI:1890473; IL20.
DR InterPro; IPR012351; Cytokine 4 hlx.
DR InterPro; IPR000098; Interleukin_10.
DR Pfam; PF00726; IL10; 1.
DR ProDom; PD003687; Interleukin_10; 1.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005515; F:interleukin-20 receptor binding; IDA.
DR GO; GO:0030097; P:hemopoiesis; NAS.
DR GO; GO:0045606; P:positive regulation of epidermal cell diffe...; TAS.
DR GO; GO:0045618; P:positive regulation of keratinocyte differe...; TAS.
DR GO; GO:0042517; P:positive regulation of tyrosine phosphoryla...; ISS.
DR GO; GO:0050727; P:regulation of inflammatory response; ISS.

```
DR   SMART; SM00188; IL10; 1.
DR   PROSITE; PS00520; INTERLEUKIN_10; 1.
KW   Cytokine; Signal.
FT   SIGNAL        1     24
FT   CHAIN        25    176       Interleukin-10.
FT   DISULFID     33    126       Potential.
FT   DISULFID     80    132       Potential.
FT   DISULFID     81    134       Potential.
SQ   SEQUENCE   176 AA;  20098 MW;  08577AF65574771 CRC64;

Query Match             73.8%;  Score 672;  DB 1;  Length 176;
Best Local Similarity   75.3%;  Pred. No. 1.5e-57;
Matches   131;  Conservative   15;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          1 MKASSLAFSLLSAAPYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSDIRGSVQAKDGNI 60
              :|  ||||.|.||.|.||||| |||||| ||||||:|||||.|.|:|||||:|||::|||
Db          1 MKGFGLAFGLFSAVGFLLWTPLTGLKTLHLGSCVITANLQAIQKEFSEIRDSVQAEDTNI 60

Qy         61 DIRILRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSFLTIK 120
              |||||||.||:|.|.::||||:|||:|:||||||:||||||:|:|||||||||||||:|| 
Db         61 DIRILRTEESLKDIKSLDRCCFLRHLVRFYLDRVFKVYQTPDHHTLRKISSLANSFLIK 120

Qy        121 KDLRLCHAHMTCHGGEEANKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEE 174
              |||..|||||:||| ||| .|:||:|||||| |||||:||||||| |||:|||| 
Db        121 KDLSVCHSHMACHGEEAMEKXYNQILSHFIELELQAAVKALGELGILLRWMEE 174
```

RESULT 3
IL19_HUMAN

```
ID   IL19_HUMAN     STANDARD;      PRT;   177 AA.
AC   Q9UHD0; Q96QR4; Q9NUA0;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Interleukin-19 precursor (IL-19) (Melanoma differentiation associated
DE   protein-like protein) (NG.1).
GN   Name=IL19; Synonyms=ZMDA1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21040165; PubMed=11196675; DOI=10.1038/sj.gene.6363714;
RA   Gallagher G., Dickensheets H., Eskdale J., Izotova L.S.,
RA   Mirochnitchenko O.V., Peat J.D., Vasquez N., Pestka S., Donnelly R.P.,
RA   Kotenko S.V.;
RT   "Cloning, expression and initial characterization of interleukin-19
RT   (IL-19), a novel homolog of human interleukin-10 (IL-10).";
RL   Genes Immun. 1:442-450(2000).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Conklin D., Petersen J., Loften-Day C., Whitmore T., Muerer M.,
RA   Sexson S., Smith D., Lok S., Powder T., O'Hara P.;
RT   "Homo sapiens homolog of melanoma differentiation associated gene.";
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RA   Kotenko S.V.;
RT   "IL-19 induces production of IL-6 and TNF-alpha and results in cell
RT   apoptosis through TNF-alpha.";
RL   J. Immunol. 169:4288-4297(2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RA   Liang Y.-C., Liu H.G., Chen F.W., Hsu J.H., Yang J.J., Chang M.-S.;
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANT PHE-175.
RA   Kotenko S.V., Pestka S.;
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
```

```
RT   PHCRC, Seattle, WA (URL: http://pga.gs.washington.edu)";
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RG   Human chromosome 1 international sequencing consortium;
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   PROTEIN SEQUENCE OF 25-39.
RA   Zhang Z., Henzel W.J.;
RX   PubMed=15340161; DOI=10.1110/ps.04682504;
RT   "Signal peptide prediction based on analysis of experimentally
RT   verified cleavage sites.";
RL   Protein Sci. 13:2819-2824(2004).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS) OF 19-177, AND DISULFIDE BONDS.
RX   PubMed=12403790; DOI=10.1074/jbc.M208602200;
RA   Chang C., Magracheva E., Kozlov S., Fong S., Tobin G., Kotenko S.,
RA   Wlodawer A., Zdanov A.;
RT   "Crystal structure of interleukin-19 defines a new subfamily of
RT   helical cytokines.";
RL   J. Biol. Chem. 278:3308-3313(2003).
CC   -!- FUNCTION: May play some important roles in inflammatory responses.
CC       Up-regulates IL-6 and TNF-alpha and induces apoptosis (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the IL-10 family.
CC   -----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   -----------------------------------------------------------------------
DR   EMBL; AF276917; AAG16755.1; -; Genomic_DNA.
DR   EMBL; AF453946; AAN40906.1; -; mRNA.
DR   EMBL; AF192498; AAF06663.1; -; mRNA.
DR   EMBL; AY040367; AAK91776.1; -; mRNA.
DR   EMBL; AF390905; AAK64498.1; -; Genomic_DNA.
DR   EMBL; AL049615; CAB72342.1; -; Genomic_DNA.
DR   PDB; 1N1F; X-ray; A=19-177.
DR   Ensembl; ENSG00000142224; Homo sapiens.
DR   HGNC; HGNC:5990; IL19.
DR   MIM; 605687; -.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0005125; F:cytokine activity; TAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   GO; GO:0007165; P:signal transduction; NAS.
DR   InterPro; IPR012351; Cytokine_4_hlx.
DR   InterPro; IPR000098; Interleukin-10.
DR   Pfam; PF00726; IL10; 1.
DR   SMART; SM00188; IL10; 1.
DR   PROSITE; PS00520; INTERLEUKIN_10; 1.
KW   3D-structure; Apoptosis; Cytokine; Direct protein sequencing;
KW   Glycoprotein; Polymorphism; Signal.
FT   SIGNAL        1     24
FT   CHAIN        25    177       Interleukin-19.
FT   CARBOHYD     56     56       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD    135    135       N-linked (GlcNAc...) (Potential).
FT   DISULFID     28    121
FT   DISULFID     75    127
FT   DISULFID     76    129
FT   VARIANT     175    175       S -> F.
FT                               /FTId=VAR_013077.
SQ   SEQUENCE   177 AA;  20392 MW;  7CCFAC22I77DB408 CRC64;

Query Match             37.1%;  Score 337.5;  DB 1;  Length 177;
Best Local Similarity   39.7%;  Pred. No. 9.4e-25;
Matches    69;  Conservative   36;  Mismatches   64;  Indels    5;  Gaps    1;

Qy          1 MKASSLAFSLLSAAPYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSDIRGSVQAKDGNI 60
              ||   |.:.|| . :||||| |  |   | ||||    . ||   | :||:||| |||:.|
Db          1 MKLQCVSLMLLGTIILLCSVDNHGLR------RCLISTDMHHIEBSFQEIRAIQAKDTFP 55
```

```
Qy   61  DIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSFLTIK 120
            ||||:|||:|||:||||||||||||||::|::||||||||||||||||||||::||::
Db   56  NVTILSTLETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKLRKISSIANSFLYMQ 115

Qy  121  KDLRLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVKALGELDILLQWMEE 174
            :::||:||||  |||||::||||||||||||||||||||||:|:|||||||:  :
Db  116  KTLRQCEQRQCHCRQEATNATRVIHDNYQLEVHAAAIKSLGELDVFLAWINK 169
```

RESULT 4
Q5VUT3_HUMAN
ID   Q5VUT3_HUMAN PRELIMINARY;   PRT;   215 AA.
AC   Q5VUT3;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Interleukin 19.
GN   Name=IL19; ORFNames=RP11-262N9.2-001;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Kay M.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
DR   EMBL; AL513315; CAH71814.1; -; Genomic_DNA.
DR   SMR; Q5VUT3; 60-215.
DR   Ensembl; ENSG00000142224; Homo sapiens.
DR   GO; GO:0005615; C:extracellular space; IEA.
DR   GO; GO:0005125; F:cytokine activity; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR000098; Interleukin-10.
DR   Pfam; PF00726; IL10; 1.
DR   PROSITE; PS00520; INTERLEUKIN_10; UNKNOWN_1.
KW   Cytokine.
SQ   SEQUENCE   215 AA;   24567 MW;   D79D6B0F11DA74E4 CRC64;

Query Match   37.1%; Score 337.5; DB 2; Length 215;
Best Local Similarity   39.7%;
Matches   69; Conservative   36; Mismatches   64; Indels   5; Gaps   1;

Qy   1 MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSDIRGSVQAKDGNI 60
            ::   : :::::::::||:::|:|:||:|:|:|||||||||::|:|:
Db   39 MKLQCVSLWLLGTLILILCSVDNHGLR----RCLISTDMHHIEESFQEIKRAIQAKDTFP 93

Qy   61 DIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSFLTIK 120
Db   94 NVTILSTLETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKLRKISSIANSFLYMQ 153

Qy 121 KDLRLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVKALGELDILLQWMEE 174
Db 154 KTLRQCEQRQCHCRQEATNATRVIHDNYQLEVHAAAIKSLGELDVFLAWINK 207
```

RESULT 5
Q4LDR4_BRARE
ID   Q4LDR4_BRARE PRELIMINARY;             PRT;   168 AA.
AC   Q4LDR4;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Interleukin 10 family protein.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Ram S., Daisuke I., Sakai M.;
RT   "Evolution of IL-10 family genes in teleosts.";
RL   Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB219579; BAE06181.1; -; mRNA.
SQ   SEQUENCE   168 AA;   19110 MW;   807D18AD736C709B CRC64;

Query Match             33.6%;  Score 306;  DB 2;  Length 168;
Best Local Similarity   42.4%;  Pred. No. 1.1e-21;
Matches   67;  Conservative   27;  Mismatches   58;  Indels   6;  Gaps   3;

```
Qy   18  LWTPSTGLKTLNLGSCVIATNLQEIRNGFSDIRGSVQAKDGNIDIRILRR--TESLQDTK 75
Db   10  LWDAAQG-RRLHLGSCKVNIHTHELRHHFQVVRQGMISGDDHKGILRLLRKDVMSSLQATE 68

Qy   76  PANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSFLTIKKDLRLRLCHAHMTCHCG 135
Db   69  ---SCCFLSQLLHFYMDTVFISYTSSHSLHRRTTSVLIANSFLSISKDLRVCHANAHCECG 125

Qy  136  EEAMKKYSQILSHFEKLEPQAAVKALGELDILLQWMEE 173
Db  126  ENTRLQLKSIQTAYEKLDQAAGTVKAIGELDSLLEWIE 163
```

RESULT 6
IL19_MOUSE
ID   IL19_MOUSE   STANDARD;   PRT;   176 AA.
AC   Q8C770;
DT   10-MAY-2005 (Rel. 47, Created)
DT   10-MAY-2005 (Rel. 47, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Interleukin-19 precursor (IL-19).
GN   Name=Il19;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE, AND FUNCTION.
RC   STRAIN=Swiss Webster / NIH;
RX   MEDLINE=22257669; PubMed=12370360;
RA   Liao Y.-C., Liang W.G., Chen F.W., Hsu J.H., Yang J.J., Chang M.-S.;
RT   "IL-19 induces production of IL-6 and TNF-alpha and results in cell
RT   apoptosis through TNF-alpha.";
RL   J. Immunol. 169:4288-4297(2002).
     -!- FUNCTION: May play some important roles in inflammatory responses.
         Up-regulates IL-6 and TNF-alpha and induces apoptosis.
     -!- SUBCELLULAR LOCATION: Secreted.
     -!- SIMILARITY: Belongs to the IL-10 family.
CC   ---
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---
DR   EMBL; AF453945; AAN40905.1; -; mRNA.
DR   HSSP; Q9UHD0; 1N1F.
DR   SMR; Q8C770; 23-170.
DR   Ensembl; ENSMUSG00000016524; Mus musculus.
DR   MGI; MGI:1890472; Il19.
DR   GO; GO:0006917; P:induction of apoptosis; IDA.
DR   GO; GO:0042226; P:interleukin-6 biosynthesis; IDA.
DR   GO; GO:0006800; P:oxygen and reactive oxygen species metabolism; IDA.
DR   InterPro; IPR000098; Interleukin-10.
DR   InterPro; IPR012351; Cytokine_4_hlx.
DR   ProDom; PD003687; Interleukin_10_1.
DR   SMART; SM00188; IL10; 1.
DR   PROSITE; PS00520; INTERLEUKIN_10; FALSE_NEG.
KW   Apoptosis; Cytokine; Glycoprotein; Signal.
FT   SIGNAL   1   24
FT   CHAIN   25   176   Interleukin-19.
FT   CARBOHYD   56   56   N-linked (GlcNAc...) (Potential).
FT   CARBOHYD   127   127   N-linked (GlcNAc...) (Potential).

Query Match   33.6%; Score 306; DB 2; Length 168;
Best Local Similarity   42.4%; Pred. No. 1.1e-21;
Matches   67; Conservative   27; Mismatches   58; Indels   6; Gaps   3;

```
Qy  136  EEAMKKYSQILSHFEKLEPQAAVKALGELDILLQWMEE 173
Db  126  ENTRLQLKSIQTAYEKLDQAAGTVKAIGELDSLLEWIE 163
```

```
FT   CARBOHYD      134    134       N-linked (GlcNAc...) (Potential).
FT   DISULFID       28    120       By similarity.
FT   DISULFID       74    126       By similarity.
FT   DISULFID       75    128       By similarity.
SQ   SEQUENCE      176 AA;  20288 MW;  73E6C1BC54077FDC CRC64;
```

```
Query Match
Best Local Similarity   30.9%;  Score 281.5;  DB 1;  Length 176;
Matches    56;  Conservative   35;  Mismatches   53;  Indels    1;  Gaps    1;

Qy    29  NLGSCVIATNLQEIRNGFSDIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLR   88
          :|.|| |.:: ::|.   :::: :: .: .|:|||||||||||| ||||:||
Db    24  SLRRCLISVDMRLIEKSFHEIKRAMOTKDTFKNVTIL-SLENLRSIKPGDVCCMTNNLLT   82

Qy    89  LYLDRVFKRNYQTPDHYTLRKISSLANSFLTIKKDLRLCHAHMTCHCGEEAMKKYSQILSH  148
          ||: ||:|||   ||||||||||||||:|| |: |:| :|| ||: : |
Db    83  FYRDRVFQDHQERSLEVLPRISSTANSFLCVQKSLERCQVHRQCNCSQBATNATRIIHDN  142

Qy   149  FEKLEPQAAVVKALGELDILLQWME  173
          |:|||:||||||||||||||| ||:
Db   143  YNQLEVSSAALKSLGELNILLAWID  167
```

```
RESULT 7
Q7SX60 TETNG
ID   Q7SX60_TETNG   PRELIMINARY;     PRT;    175 AA.
AC   Q7SX60;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Interleukin-20.
GN   Name=IL20;
OS   Tetraodon nigroviridis (Green puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetraodontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=99883;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=12862921; DOI=10.1186/1471-2164-4-29;
RA   Lutfalla G., Crollius H.R., Stange-Thomann N., Jaillon O.,
RA   Mogensen K., Monneron D.;
RT   "Comparative genomic analysis reveals independent expansion of a
RT   lineage-specific gene family in vertebrates: The class II cytokine
RT   receptors and their ligands in mammals and fish.";
RL   BMC Genomics 4:29-29(2003).
DR   EMBL; AY294557; AAP57414.1; -; Genomic_DNA.
DR   EMBL; AY294558; AAP57416.1; -; mRNA.
DR   GO; GO:0005615; C:extracellular space; IEA.
DR   GO; GO:0005125; F:cytokine activity; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR012351; Cytokine_4_hlx.
DR   InterPro; IPR000098; Interleukin_10.
DR   Pfam; PF00726; IL10; 1.
DR   ProDom; PD003687; Interleukin_10; 1.
DR   SMART; SM00188; IL10; 1.
SQ   SEQUENCE    175 AA;  19838 MW;  DE6FA67B0038E034 CRC64;
```

```
Query Match
Best Local Similarity   29.3%;  Score 266.5;  DB 2;  Length 175;
Matches    57;  Conservative   33;  Mismatches   53;  Indels    7;  Gaps    3;

Qy    26  KTLNLGSCVIATNLQEIRNGFSDIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRH   85
          :|| ||:| |:|| |:||||| |||||:||||||||||||||||||||| |:||||||
Db    24  QTLLVDSCSISADLQEMHQHHSNIRLNAITEDEBIGVKLLSK-RLMEDVQDGQRCCFLRL   82

Qy    86  LLRLYLDRVFKRNYQTPDHYTLRKISSLANSFLTI--KKDLRLCHAHMTCHCGEEAMKKYS  143
          :|:|:|:|:| :||||||||||||||:||||||    |||:||||||||||| || :
Db    83  VLQFYIDKVPPSYLSSHPQNQSSSSLANTFIIIVRKQMIQKCH----CLCBEQETQKKVD  138
```

```
Db   139  SLLDAFNKLEASKAVLKAVGELDTVLQWIQ  168
```

```
RESULT 8
Q92523 MOUSE
ID   Q92523_MOUSE   PRELIMINARY;     PRT;    220 AA.
AC   Q92523;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Th2-specific cytokine FISP.
GN   Name=Il24;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=BALB/c;
RX   MEDLINE=21240641; PubMed=11342597;
RA   Schaefer G., Venkataraman C., Schindler U.;
RT   "FISP (IL-4-induced secreted protein), a novel cytokine-like molecule
RT   secreted by Th2 cells.";
RL   J. Immunol. 166:5859-5863(2001).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
DR   EMBL; AF333251; AAK52470.1; -; mRNA.
DR   Ensembl; ENSMUSG00000026420; Mus musculus.
DR   MGI; MGI:2135548; Il24.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   InterPro; IPR000098; Interleukin_10.
DR   SMART; SM00188; IL10; 1.
DR   ProDom; PD003687; Interleukin_10; 1.
DR   PROSITE; PS00520; INTERLEUKIN_10; 1.
KW   Cytokine.
SQ   SEQUENCE    220 AA;  25168 MW;  5BF76C8612AC909D CRC64;
```

```
Query Match
Best Local Similarity   24.4%;  Score 222;  DB 2;  Length 220;
Matches    56;  Conservative   30;  Mismatches   71;  Indels    6;  Gaps    4;

Qy    17  LLWTPSTGL--KTLNLGSC-VIATNLQEIRNGFSDIRGSVQAKDGNIDIRILRRTESLQD   73
          |||   || :|| ||:|  |: || |:|||||:|||||:||| : ||:|||||||||
Db    55  LLWNQVPGLEGQEPRFGSCCQVTGVVLPELWEAFWTVKNTVQTQDDITSIRLL-KPQVLRN  113

Qy    74  TKPANRCCLLRHLLRLYLDRVFKRNYQT--PDHYTLRKISSLANSFLTIKKDLRLCHAHMT  131
          ||| |||| :|||| |: ||:| :|:|   |||||||||:||||||| | |:| :|||||
Db   114  VSGASSCYLAHSLLKFYLNTVFKNYHSKIAKFKVLRSFSTLANNFIVIMSQLQPSKDNSM  173

Qy   132  CHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEE  174
          || :||| :|: ||  |:|||||||:||||||||||| |::
Db   174  LPISESAHQRFLLFRRAFKQLDTEVALVKAFGEVDILLTWMQK  216
```

```
RESULT 9
Q92S4 MOUSE
ID   Q92S4_MOUSE   PRELIMINARY;     PRT;    181 AA.
AC   Q92S4;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Melanoma differentiation associated gene-7.
GN   Name=Il24;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=129/SvJ;
RA   Madireddi M.T., Lin J., Su Z., Shay J.W., Huberman E., Fisher P.B.;
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
```

```
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
DR   EMBL; AF235006; AAK52590.1; -; mRNA.
DR   Ensembl; ENSMUSG00000026420; Mus musculus.
DR   MGI; MGI:2135548; Il24.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   InterPro; IPR000098; Interleukin_10.
DR   ProDom; PD003687; Interleukin_10; 1.
DR   SMART; SM00188; IL10; 1.
DR   PROSITE; PS00520; INTERLEUKIN_10; 1.
KW   Cytokine.
SQ   SEQUENCE   181 AA;  20812 MW;  05CA43872D53D555 CRC64;

Qy  Query Match             24.2%;  Score 220;  DB 2;  Length 181;
    Best Local Similarity   34.4%;  Pred. No. 3.2e-13;
    Matches   56;  Conservative   30;  Mismatches   71;  Indels   6;  Gaps   4;

Qy    17  LLWTPSTGL--KTLNLGSC-VIATNLQEIRNGFSDIRGSVYQAKDGNIDIRILRRTESLQD  73
              |||   : || :      |:: |   ||  ::| |||| ||| |:|   |:||  ||| ::
Db    16  LLWNQVPGLEGQEFRSGSCCQVTGVVLPELWEAFWTVKNIVQTQDDITSIRLL-KPQVLRN  74

Qy    74  TKPANRCCLLRHLLRLYLDRVFKNYQT--PDHYTLRKISSLANSFLTIKQDLRLCHAHMT  131
              ||| | ||  || |||| | |:| ||    |  | ||:|| | |: |  :| | || ||
Db    75  VSGAESCYLAHSLLKFYLNTVFKNYHSKIAKFKVLRSFSTLANNFIVIMSQLQPSKDNSM  134

Qy   132  CHCGEEAMKKYSQILSHPEKLEPQAAVVKALGELDILLQWMEE  174
               ||   |:|| | | : || :|  |  |  ||  |||::  |
Db   135  LPISESAHQRFLLFRRAFKQLDTEVALVKAFGEVDILLTWMQK  177
```

```
RESULT 10
IL24_HUMAN

ID   IL24_HUMAN              STANDARD;      PRT;    206 AA.
AC   Q13007; Q96DB0; Q96KG4;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Interleukin-24 precursor (Suppression of tumorigenicity 16 protein)
DE   (Melanoma differentiation-associated protein 7) (MDA-7).
GN   Name=IL24; Synonyms=MDA7, ST16;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Melanoma;
RX   MEDLINE=96132699; PubMed=8545104;
RA   Jiang H., Lin J.J., Su Z.-Z., Goldstein N.I., Fisher P.B.;
RT   "Subtraction hybridization identifies a novel melanoma differentiation
RT   associated gene, mda-7, modulated during human melanoma
RT   differentiation, growth and progression.";
RL   Oncogene 11:2477-2486(1995).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS HIS-124; ARG-125 AND
RP   LEU-131.
RA   Rieder M.J., Armel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA   Peel C.L., Toth E.J., Yi Q., Nickerson D.A.;
RT   "SeattleSNPs, NHLBI HL66682 program for genomic applications, UW-
RT   FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE, AND VARIANT HIS-124.
RC   TISSUE=Fibroblast;
RA   Madireddi M.T., Lin J., Su Z.-Z., Shay J.W., Huberman E., Fisher P.B.;
RT   "Genomic structure, chromosomal localization and expression of
RT   melanoma differentiation associated gene-7 (mda-7): potential
RT   relationship with cellular senescence.";
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RL   Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [6]
RP   PROTEIN SEQUENCE OF 52-66.
RX   PubMed=15340161; DOI=10.1110/ps.04682504;
RA   Zhang Z., Henzel W.J.;
RT   "Signal peptide prediction based on analysis of experimentally
RT   verified cleavage sites.";
RL   Protein Sci. 13:2819-2824(2004).
RN   [7]
RP   CHARACTERIZATION.
RX   MEDLINE=99045696; PubMed=9826712; DOI=10.1073/pnas.95.24.14400;
RA   Su Z.-Z., Madireddi M.T., Lin J.J., Young C.S.H., Kitada S.,
RA   Reed J.C., Goldstein N.I., Fisher P.B.;
RT   "The cancer growth suppressor gene mda-7 selectively induces apoptosis
RT   in human breast cancer cells and inhibits tumor growth in nude mice.";
RL   Proc. Natl. Acad. Sci. U.S.A. 95:14400-14405(1998).
CC   -!- FUNCTION: Has antiproliferative properties in human melanoma cells
CC       and may contribute to terminal cell differentiation. May also
CC       function as a negative regulator of melanoma progression.
CC       Formation in vivo in nude mice. They found that it selectively
CC       induces apoptosis in human breast cancer cells.
CC   -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC   -!- TISSUE SPECIFICITY: Up-regulated in melanoma cells induced to
CC       terminally differentiate.
CC   -!- SIMILARITY: Belongs to the IL-10 family.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; U16261; AAA91780.1; -; mRNA.
DR   EMBL; AF276916; AAG41401.1; -; Genomic_DNA.
DR   EMBL; AF235005; AAK52589.1; -; Genomic_DNA.
DR   EMBL; AY062931; AAL34146.1; -; Genomic_DNA.
DR   EMBL; BC009681; AAH09681.1; -; mRNA.
DR   Ensembl; ENSG00000162892; Homo sapiens.
DR   HGNC; HGNC:11346; IL24.
DR   H-InvDB; HIX0001532; -.
DR   MIM; 604136; -.
DR   GO; GO:0006915; P:apoptosis; TAS.
DR   InterPro; IPR012351; Cytokine_4_hlx.
DR   InterPro; IPR000098; Interleukin_10.
DR   ProDom; PD003687; Interleukin_10; 1.
DR   SMART; SM00188; IL10; 1.
DR   PROSITE; PS00520; INTERLEUKIN_10; 1.
KW   Apoptosis; Cytokine; Direct protein sequencing; Glycoprotein;
KW   Polymorphism; Signal.
```

```
FT   SIGNAL          1     51
FT   CHAIN          52    206                 Interleukin-24.
FT   CARBOHYD       85     85                 N-linked (GlcNAc...)  (Potential).
FT   CARBOHYD       99     99                 N-linked (GlcNAc...)  (Potential).
FT   CARBOHYD      126    126                 N-linked (GlcNAc...)  (Potential).
FT   CARBOHYD      124    124                 N-linked (GlcNAc...)  (Potential).
FT   VARIANT       125    125                 H -> R (in dbSNP:3093431).
FT                                            /FTId=VAR_011974.
FT   VARIANT       125    125                 H -> R (in dbSNP:3093431).
FT                                            /FTId=VAR_013097.
FT   VARIANT       131    131                 V -> L (in dbSNP:3093446).
FT                                            /FTId=VAR_013098.
FT   CONFLICT       14     14                 A -> AS (in Ref. 4).
FT   SEQUENCE      206 AA;  23825 MW;  CB8135083EAB8DDD CRC64;

Query Match             23.8%;  Score 217;  DB 1;  Length 206;
Best Local Similarity   32.8%;  Pred. No. 7.3e-13;
Matches  57;  Conservative  39;  Mismatches  66;  Indels  12;  Gaps  5;

Qy          6  LAFSILSAAFYLLWTPSTGL--KTLNLGSCVIATNL-QEIRNGFSDIRGSVQAKDGNIDI 62
               ||:|      :|:|: |||  :  ||:   ||| ||  :: ::||||||:
Db         36  LGFTL-----LLWSQVSGAQGQEFHFGPCQVKGVVPQKLWEAFWAVKDTMQAQDNITSA 89

Qy         63  RILRRTESLQDTKPANRCCLLRHILRLYLDRVFKNY--QTPDHYTLRKISSLANSFLTIK 120
               |:||:||  :::|||  ::| |||::|| :|:: ||   :||::|:|||| ||| ||:|:
Db         90  RLLQQ-EVLQNVSDAESCYLVHTLLEFYLKTVFKNYHNRTVEVRTLKSFSTLANNFVLIV 148

Qy        121  KDLRLCHAHMTCHGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEE 174
               :|||| :| | ||  :|||||||:||||: ||||||: :||| |||| :|
Db        149  SQLQPSQENEMFSIRDSAHRRFLLFRRAFKQLDVEAALTKALGEVDILLTWMQK 202

RESULT 11
ID   Q53X27_HUMAN  PRELIMINARY;  PRT;  207 AA.
AC   Q53X27;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Interleukin 24.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA   Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA   Phelan M., Farmer A.;
RT   "Cloning of human full-length CDSs in BD Creator(TM) System Donor
RT   vector.";
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
DR   EMBL; BT007156; AAP35820.1; -; mRNA.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0005125; F:cytokine activity; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
KW   Cytokine.
SQ   SEQUENCE      207 AA;  23912 MW;  17687A467B9CB551 CRC64;

Query Match             23.8%;  Score 217;  DB 2;  Length 207;
Best Local Similarity   32.8%;  Pred. No. 7.4e-13;
Matches  57;  Conservative  39;  Mismatches  66;  Indels  12;  Gaps  5;

Qy          6  LAFSILSAAFYLLWTPSTGL--KTLNLGSCVIATNL-QEIRNGFSDIRGSVQAKDGNIDI 62
               ||:|      :|:|: |||  :  ||:   ||| ||  :: ::||||||:
Db         37  LGFTL-----LLWSQVSGAQGQEFHFGPCQVKGVVPQKLWEAFWAVKDTMQAQDNITSA 90

Qy         63  RILRRTESLQDTKPANRCCLLRHILRLYLDRVFKNY--QTPDHYTLRKISSLANSFLTIK 120
               |:||:||  :::|||  ::| |||::|| :|:: ||   :||::|:|||| ||| ||:|:
Db         91  RLLQQ-EVLQNVSDAESCYLVHTLLEFYLKTVFKNYHNRTVEVRTLKSFSTLANNFVLIV 149

Qy        121  KDLRLCHAHMTCHGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEE 174
               :|||| :| | ||  :|||||||:||||: ||||||: :||| |||| :|
Db        150  SQLQPSQENEMFSIRDSAHRRFLLFRRAFKQLDVEAALTKALGEVDILLTWMQK 203

RESULT 12
ID   MOB5_RAT  STANDARD;  PRT;  183 AA.
AC   Q9JI24;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Cytokine-like protein Mob-5 precursor.
GN   Name=Mob5;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20387329; PubMed=10825166; DOI=10.1074/jbc.M001958200;
RA   Zhang R., Tan Z., Liang P.;
RT   "Identification of a novel ligand-receptor pair constitutively
RT   activated by ras oncogene.";
RL   J. Biol. Chem. 275:24436-24443(2000).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the IL-10 family.
CC   -------------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   -------------------------------------------------------------------------
DR   EMBL; AF269251; AAF75553.1; -; mRNA.
DR   Ensembl; ENSRNOG00000004470; Rattus norvegicus.
DR   GO; GO:0048144; P:fibroblast proliferation; TAS.
DR   GO; GO:0042060; P:wound healing; TAS.
DR   InterPro; IPR012351; Cytokine_4_hlx.
DR   InterPro; IPR000098; Interleukin_10.
DR   ProDom; PD003687; Interleukin-10.
DR   SMART; SM00188; IL10; 1.
DR   PROSITE; PS00520; INTERLEUKIN_10; 1.
KW   Cytokine; Glycoprotein; Signal.
FT   SIGNAL          1     28
FT   CHAIN          29    183                 Cytokine-like protein Mob-5.
FT   CARBOHYD       76     76                 N-linked (GlcNAc...) (Potential).
SQ   SEQUENCE      183 AA;  21096 MW;  AF7A1146GC491AC4 CRC64;

Query Match             21.0%;  Score 191;  DB 1;  Length 183;
Best Local Similarity   33.1%;  Pred. No. 2.2e-10;
Matches  49;  Conservative  31;  Mismatches  60;  Indels  8;  Gaps  5;

Qy         31  GSC-VIATNL-QEIRNGFSDIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHILRL 89
               |:| |  |:||: :||:|::||||||:  |:|:||||||: |: |||  ::| |||::|:
Db         34  GPCQVTGVVLPELWEAFWTVKNTVKIQDELTSVRLL-KPQVLQNVSDAESCYLAHSLLKF 92

Qy         90  YLDRVFKNYQTP--DHYTLRKISSLANSFLTIKKDLRLCHAHMTCHGEEAMKKYSQILS 147
               ||: |||||  :  ||||||||| :|| ||:|  ||| | |  |  :|||||||:||
Db         93  YLNTVFKNYHSKIVKPFVLKSFSTLANNFLVIMSKLQPSKDNAMLPISDSARRRF--LLY 150

Qy        148  H--FEKLEPQAAVVKALGELDILLQWMEE 173
               |   |||:  || ||:||| ||||:||:
Db        151  HRTFKQLDIEVALAXAFGEVDILLAWMQ 178

RESULT 13
ID   Q9WP8_RAT  PRELIMINARY;  PRT;  183 AA.
AC   Q9WP8;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
```

```
DE   C49a.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=99308986; PubMed=10381256;
RX   DOI=10.1002/(SICI)1097-4644(19990701)74:1<1:1>AID-JCB1>3.3.CO;2-D;
RA   Soo C., Shaw W.W., Freymiller E., Longaker M.T., Bertolami C.N.,
RA   Chiu R., Tieu A., Ting K.;
RT   "Cutaneous rat wounds express c49a, a novel gene with homology to the
RT   human melanoma differentiation associated gene, mda-7.";
RL   J. Cell. Biochem. 74:1-10(1999).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
DR   EMBL; AF004774; AAB69171.1; -; mRNA.
DR   ProDom; PD003687; Interleukin_10; 1.
DR   PROSITE; PS00520; INTERLEUKIN_10; 1.
KW   Cytokine.
SQ   SEQUENCE   183 AA;   21052 MW;   F69A96AFC473E4F CRC64;

Query Match       20.5%;  Score 187;  DB 2;  Length 183;
Best Local Similarity   32.3%;  Pred. No. 5.5e-10;
Matches   47;  Conservative   29;  Mismatches   66;  Indels   4;  Gaps   3;

Qy   31 GSC-VIATNLQEIRNGFSDIRGSVQAAKDGNIDIDIRIRLRRTESLQDTKPANRCCLLRHLLRL 89
Db   34 GPCQVTGVVLPELWEAFWTVKNTVKTQDELTSARLL-KPQVLQNVSDAESCYLAHSLLKP 92

Qy   90 -DHYTLRKISSLANSFLTIKKDLRLRLCHAHMTCHCGEEAMKKYSQILS 147
Db   93 YLNTVFKNYHSKIVKFVLKSFSTLANNFLVIMSKLQPSKDNAMLPISDSARRRFLLFHR 152

Qy  148 HFEKLEPQAAVVKALGELDILLQWME 173
Db  153 TFKQLDIEVALAKAFGEVDILLAWMQ 178


RESULT 14
ID   Q6A2H5_CHICK
AC   Q6A2H5;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Interleukin-10.
GN   Name=IL-10;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Rothwell L., Young J., Zoorob R., Whittaker C.A., Hesketh P.,
RA   Archer A., Smith A.L., Kaiser P.;
RT   "Cloning and Characterization of Chicken IL-10 and Its Role in the
RT   Immune Response to Eimeria maxima.";
RL   J. Immunol. 173:2675-2682(2004).
DR   EMBL; AJ621254; CAF18432.1; -; mRNA.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0005125; F:cytokine activity; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR000098; Interleukin-10.
DR   Pfam; PF00726; IL10; 1.
```

```
DR   PRINTS; PR01294; INTRLEUKIN10.
DR   ProDom; PD003687; Interleukin_10; 1.
DR   SMART; SM00188; IL10; 1.
SQ   SEQUENCE   175 AA;   20514 MW;   B0966EBEAFDFB050 CRC64;

Query Match       19.3%;  Score 175.5;  DB 2;  Length 175;
Best Local Similarity   30.3%;  Conservative   32;  Mismatches   81;  Indels   9;  Gaps   5;
Matches   53;

Qy    1 MKASSLAFSILLSAAFYLLWTPSTGLKTINLG-SCVIATNLQEIRNGFSDIRGSVQAKDGN 59
Db    1 MQTCCQALILLLAACTL---PAHCLEPTCLHFSELLPARLRELRVKFEEIKDYFQSRDDE 57

Qy   60 IDIRIRLRRTESLQDTKPANRCCLLRHLLRLIRYLDRVFKNYQTPDHYTLRKISSLANSFLTI 119
Db   58 LNIQLL-SSELLDEFKGTFGCQQSVSEMLRFYTDEVLPRAMQTSTSHQQSMGDLGNMLLGL 116

Qy  120 KKDLRLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWME 174
Db  117 KATMRRCHRFFTC---EKRSKAIKQIKETFEKMD-ENGIYKAMGEFDIFINYIEE 167


RESULT 15
ID   Q6A2H4_CHICK
AC   Q6A2H4;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Interleukin-10.
GN   Name=IL10;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Rothwell L., Young J., Zoorob R., Whittaker C.A., Hesketh P.,
RA   Archer A., Smith A.L., Kaiser P.;
RT   "Cloning and Characterization of Chicken IL-10 and Its Role in the
RT   Immune Response to Eimeria maxima.";
RL   J. Immunol. 173:2675-2682(2004).
DR   EMBL; AJ621614; CAF21727.1; -; Genomic DNA.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0005125; F:cytokine activity; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR012351; Cytokine 4_hlx.
DR   InterPro; IPR012352; IL-10_add_helix.
DR   InterPro; IPR000098; Interleukin-10.
DR   Pfam; PF00726; IL10; 1.
DR   PRINTS; PR01294; INTRLEUKIN10.
DR   ProDom; PD003687; Interleukin_10; 1.
DR   SMART; SM00188; IL10; 1.
SQ   SEQUENCE   175 AA;   20496 MW;   A4966ABAAFDFB057 CRC64;

Query Match       19.3%;  Score 175.5;  DB 2;  Length 175;
Best Local Similarity   30.3%;  Conservative   32;  Mismatches   81;  Indels   9;  Gaps   5;
Matches   53;

Qy    1 MKASSLAFSILLSAAFYLLWTPSTGLKTINLG-SCVIATNLQEIRNGFSDIRGSVQAKDGN 59
Db    1 MQTCCQALILLLAACTL---PAHCLEPTCLHFSELLPARLRELRVKFEEIKDYFQSRDDE 57

Qy   60 IDIRIRLRRTESLQDTKPANRCCLLRHLLRLIRYLDRVFKNYQTPDHYTLRKISSLANSFLTI 119
Db   58 LNIQLL-SSELLDEFKGTFGCQQSVSEMLRFYTDEVLPRAMQTSTSHQQSMGDLGNMLLGL 116

Qy  120 KKDLRLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEE 174
Db  117 KATIRRCHRFFTC---EKRSKAIKQIKETFEKMD-ENGIYKAMGEFDIFINYIEE 167
```

us-10-789-129-2.rup

Search completed: December 24, 2005, 10:46:54
Job time : 230 secs

This Page Blank (uspto)

OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: December 28, 2005, 13:49:18 ; Search time 2943 Seconds
(without alignments)
2781.331 Million cell updates/sec

Title: US-10-789-129-26
Perfect score: 753
Sequence: 1 CVIATNLQEIRNGFSDIRGS........AVVKALGELDILLQWMEETE 144

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop   6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 5883141 seqs, 2842172S653 residues
                 Listing first 45 summaries

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2 1/USPTO spool_p/US10789129/runat 23122005 152720 20263/app query.fasta_1.327
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.tge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10789129 @CGN 1 1 7415 @runat 23122005 152720 20263 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   GenEmbl:*
                 1: gb_ba:*
                 2: gb_in:*
                 3: gb_env:*
                 4: gb_om:*
                 5: gb_ov:*
                 6: gb_pat:*
                 7: gb_ph:*
                 8: gb_pr:*
                 9: gb_ro:*
                10: gb_sts:*
                11: gb_sy:*
                12: gb_un:*
                13: gb_vi:*
                14: gb_htg:*
                15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	753	100.0	926	6	BD087297	BD087297 Mammalian
2	753	100.0	926	6	CQ818183	CQ818183 Sequence
3	753	100.0	926	6	CS109174	CS109174 Sequence

4	753	100.0	926	8	CS110179	CS110179 Sequence
5	753	100.0	926	6	AR342856	AR342856 Sequence
6	753	100.0	926	8	AP224266	AP224266 Homo sapi
7	749	99.5	462	6	CS123418	CS123418 Sequence
8	749	99.5	531	6	BC069311	BC069311 Homo sapi
9	749	99.5	531	6	BC069364	BC069364 Homo sapi
10	749	99.5	531	6	BC069398	BC069398 Homo sapi
11	749	99.5	531	6	BC069425	BC069425 Homo sapi
12	749	99.5	531	6	BC069449	BC069449 Homo sapi
13	749	99.5	531	6	BC069487	BC069487 Homo sapi
14	749	99.5	531	6	BC069523	BC069523 Homo sapi
15	749	99.5	531	6	BC069559	BC069559 Homo sapi
16	749	99.5	531	11	AY885562	AY885562 Synthetic
17	749	99.5	531	11	AY891211	AY891211 Synthetic
18	749	99.5	531	11	AY893295	AY893295 Synthetic
19	749	99.5	603	8	BC074948	BC074948 Homo sapi
20	749	99.5	603	8	BC074949	BC074949 Homo sapi
21	749	99.5	867	6	AX498605	AX498605 Sequence
22	749	99.5	867	6	AX537938	AX537938 Sequence
23	746	99.1	926	6	CQ889881	CQ889881 Sequence
24	746	99.1	926	6	CQ889943	CQ889943 Sequence
25	739	98.1	1571	6	CQ970652	CQ970652 Sequence
26	739	98.1	1571	6	CS133455	CS133455 Sequence
27	739	98.1	1571	8	AX092406	AX092406 Sequence
28	739	98.1	1571	6	AX359964	AX359964 Sequence
29	739	98.1	1571	6	AX362457	AX362457 Sequence
30	739	98.1	1571	6	AX376542	AX376542 Sequence
31	739	98.1	1571	6	AX454700	AX454700 Sequence
32	739	98.1	1571	6	AX463964	AX463964 Sequence
33	739	98.1	1571	6	AX464412	AX464412 Sequence
34	739	98.1	1571	6	AX491178	AX491178 Sequence
35	739	98.1	1571	6	AX697333	AX697333 Sequence
36	739	98.1	1571	8	AY358320	AY358320 Homo sapi
37	686	91.1	747	6	BD087304	BD087304 Mammalian
38	686	91.1	747	6	CQ818192	CQ818192 Sequence
39	686	91.1	747	6	CS109203	CS109203 Sequence
40	686	91.1	747	6	CS112208	CS112208 Sequence
41	686	91.1	747	6	AR342863	AR342863 Sequence
42	587.5	78.0	793	6	BD087298	BD087298 Mammalian
43	587.5	78.0	793	6	CQ818185	CQ818185 Sequence
44	587.5	78.0	793	6	CS109177	CS109177 Sequence
45	587.5	78.0	793	6	CS110182	CS110182 Sequence

ALIGNMENTS

RESULT 1
BD087297

LOCUS   BD087297   926 bp   DNA   linear   PAT 27-AUG-2002
DEFINITION   Mammalian cytokine-like polypeptide-10.
ACCESSION   BD087297
VERSION   BD087297.1 GI:22632907
KEYWORDS   JP 200152413I-A/1.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominidae; Homo.
REFERENCE   1 (bases 1 to 926)
AUTHORS   Conklin,D.C., Haldeman,B.A. and Grossmann,A.
TITLE   Mammalian cytokine-like polypeptide-10
JOURNAL   Patent: JP 200152413I-A 1 04-DEC-2001;
ZYMOGENETICS INC
COMMENT   OS   Homo sapiens (human)
             PN   JP 200152413I-A/1
             PD   04-DEC-2001
             PF   25-NOV-1998 JP 2000522245
             PR   26-NOV-1997 US 08/979156
             PI   DARRELL C CONKLIN, BETTY A HALDEMAN, ANGELIKA GROSSMANN PC
             C12N15/09,A01K67/027,A61K38/00,A61K48/00,A61P1/00, PC
             A61P17/00,
             PC   A61P35/00,A61P37/02,A61P43/00,C07K14/52,C07K16/24,C07K16/42,
             PC   C12N15/00,

FEATURES
  source

PC A61K37/02
CC Mammalian cytokine-like polypeptide-10
FH
FT CDS

  1..926
  /organism="Homo sapiens"
  /mol_type="genomic DNA"
  /db_xref="taxon:9606"

ORIGIN

Location/Qualifiers
(45)..(572).

Location/Qualifiers

/mol_type="unassigned DNA"
/db_xref="taxon:9606"
45..575
/note="unnamed protein product"

CDS

ORIGIN

/mol_type="unassigned DNA"
/db_xref="taxon:9606"
45..575
/note="unnamed protein product"
/codon_start=1
/protein_id=
/db_xref="GI:48426976.1"
/translation="MKASSLAFSLLSAAPYLLMTPSTGLKTLNIGSCVIATNLQEIRN
GFSDIRGSVQAKDGNIDIRILRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPD
HYTLRKISSLANSFLTIKKDLRLCHAHMTCHCGEEAMKKYSQIILSHFEKLEPQAAVVK
ALGELDILLQWMEETE"

Alignment Scores:

Pred. No.:
Score: 753.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 6
DB:

Length: 926
Matches: 144
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

3.22e-72

US-10-789-129-26 (1-144) x BD087297 (1-926)

```
Qy      1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    141 TGTGTGATCGCCACAAACCTTCAGGAAATCAGAAATGGATTTTCTGACAATACGGGCAGT 200

Qy     21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgAsnTyrGluSerLeuGln 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    201 GTGCAAGCCAAAGATGGAAACATTGACATCAGAAATCTTAAGGAGGACTCGAGTCTTTGCAA 260

Qy     41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    261 GACACAAAGCCTGCGAATCGATGTGCCTCCTGCGCCATTTGCTAAGGACTCTACTGGAC 320

Qy     61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    321 AGGGTATTTAAAAACTACCAGACCCCGACCATTATAACTCTCCGGAAGATCAGCAGCCTC 380

Qy     81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    381 GCCAATTCCTTCTTTACCATCAAGAAGGACCTCCGGCTCTGTCATGCCCACATGACATGC 440

Qy    101 HisCysGlyGluGluAlaMetLysLysTyrSerGlnIleIleLeuSerHisPheGluLysLeu 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    441 CATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG 500

Qy    121 GluProGlnAlaAlaValValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    501 GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATG 560

Qy    141 GluGluThrGlu 144
            |||||||||
Db    561 GAGGAGACAGAA 572
```

RESULT 2

LOCUS CQ81818 3
  CQ81818 3 926 bp DNA linear PAT 07-JUN-2004
DEFINITION Sequence 1 from Patent EP1424393.
ACCESSION CQ81818 3
VERSION CQ81818 3.1 GI:48426975
KEYWORDS
SOURCE Homo sapiens (human)
  ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Hominidae; Homo.
REFERENCE 1
  AUTHORS Conklin,D.C., Haldeman,B.A. and Grossmann,A.
  TITLE Mammalian cytokine-like polypeptide-10
  JOURNAL Patent: EP 1424393-A 1 02-JUN-2004;
  Zymogenetics Inc (US)

FEATURES
  source

Location/Qualifiers
  1..926
  /organism="Homo sapiens"

RESULT 3

LOCUS CS109174
  CS109174 926 bp DNA linear PAT 22-JUN-2005
DEFINITION Sequence 1 from Patent WO200505 2001.
ACCESSION CS109174
VERSION CS109174.1 GI:68148023
KEYWORDS
SOURCE Homo sapiens (human)
  ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Hominidae; Homo.
REFERENCE 1
  AUTHORS Xu,W., Kindsvogel,W.R., Chen,Z., Hughes,S.D., Chandrasekher,Y.A.,
  Dillon,S.R., Lehner,J.M., Siadak,A.W., Sivakumar,P.V. and
  Moore,M.D.
  TITLE Anti-il-20 receptor antibodies and binding partners and methods of
  using in inflammation

Alignment Scores:

Pred. No.:
Score: 753.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 6
DB:

Length: 926
Matches: 144
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

3.22e-72

US-10-789-129-26 (1-144) x CQ81818 3 (1-926)

```
Qy      1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    141 TGTGTGATCGCCACAAACCTTCAGGAAATCAGAAATGGATTTTCTGACAATACGGGCAGT 200

Qy     21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgAsnTyrGluSerLeuGln 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    201 GTGCAAGCCAAAGATGGAAACATTGACATCAGAAATCTTAAGGAGGACTCGAGTCTTTGCAA 260

Qy     41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    261 GACACAAAGCCTGCGAATCGATGTGCCTCCTGCGCCCCATTTGCTAAGGACTCTACTGGAC 320

Qy     61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    321 AGGGTATTTAAAAACTACCAGACCCCGACCATTATAACTCTCCGGAAGATCAGCAGCCTC 380

Qy     81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    381 GCCAATTCCTTCTTTACCATCAAGAAGGACCTCCGGCTCTGTCATGCCCACATGACATGC 440

Qy    101 HisCysGlyGluGluAlaMetLysLysTyrSerGlnIleIleLeuSerHisPheGluLysLeu 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    441 CATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG 500

Qy    121 GluProGlnAlaAlaValValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    501 GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATG 560

Qy    141 GluGluThrGlu 144
            |||||||||
Db    561 GAGGAGACAGAA 572
```

FEATURES
  source
Location/Qualifiers
  1..926
  /organism="Homo sapiens"

JOURNAL   Patent: WO 200505201-A 1 09-JUN-2005;
          ZymoGenetics, Inc. (US)
FEATURES   Location/Qualifiers
     source   1..926
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     CDS   45..575
                     /codon_start=1
                     /protein_id="CAJ09892.1"
                     /db_xref="GI:68148024"
                     /note="unnamed protein product"
                     /translation="MKASSLAFSLLSAAFYLLWTPSTGLKTLNIGSCVIATNLQEIRN
                     GFSDIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPD
                     HYTLRKISSLANSFLTIKKDLRLCHAHMTHCGEEAMKKYSQILSHFEKLEPQAAVVK
                     ALGELDILLQWMEETE"
ORIGIN

US-10-789-129-26 (1-144) x CS109174 (1-926)

Alignment Scores:
Pred. No.:
Score: 3.22e-72   Length: 926
                          753.00   Matches: 144
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 6   Indels: 0
DB: Gaps: 0

Qy   1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
Db 141 TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGACATACGGGGCAGT 200

Qy   21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
Db 201 GTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAA 260

Qy   41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
Db 261 GACACAAAGCCTGCGAATCGATGCTGCCTCCTCCGCCATTTGCTAAGGACTTCTATCTGGAC 320

Qy   61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
Db 321 AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC 380

Qy   81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
Db 381 GCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTGCATGCCCCACATGACATGC 440

Qy 101 HisCysGlyGluGluAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu 120
Db 441 CATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG 500

Qy 121 GluProGlnAlaAlaValValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet 140
Db 501 GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATG 560

Qy 141 GluGluThrGlu 144
Db 561 GAGGAGACAGAA 572

RESULT 4
LOCUS   CS110179   926 bp   DNA   linear   PAT 22-JUN-2005
DEFINITION Sequence 1 from Patent WO200505200O.
ACCESSION   CS110179
VERSION   CS110179.1   GI:68148437
KEYWORDS
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1

AUTHORS   Xu,W., Kindsvogel,W.R., Chen,Z., Hughes,S.D., Chandrasekher,Y.A.,
          Dillon,S.R., Lehner,J.M., Siadak,A.W., Sivakumar,P.V. and
          Moore,M.D.
TITLE   Anti-il-20 antibodies and binding partners and methods of using in
          inflammation
JOURNAL   Patent: WO 200505200-A 1 09-JUN-2005;
          ZymoGenetics, Inc. (US)
FEATURES   Location/Qualifiers
     source   1..926
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     CDS   45..575
                     /codon_start=1
                     /note="unnamed protein product"
                     /protein_id="CAJ09906.1"
                     /db_xref="GI:68148438"
                     /translation="MKASSLAFSLLSAAFYLLWTPSTGLKTLNIGSCVIATNLQEIRN
                     GFSDIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPD
                     HYTLRKISSLANSFLTIKKDLRLCHAHMTHCGEEAMKKYSQILSHFEKLEPQAAVVK
                     ALGELDILLQWMEETE"
ORIGIN

US-10-789-129-26 (1-144) x CS110179 (1-926)

Alignment Scores:
Pred. No.:
Score: 3.22e-72   Length: 926
                          753.00   Matches: 144
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 6   Indels: 0
DB: Gaps: 0

Qy   1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
Db 141 TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGACATACGGGGCAGT 200

Qy   21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
Db 201 GTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAA 260

Qy   41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
Db 261 GACACAAAGCCTGCGAATCGATGCTGCCTCCTCCGCCATTTGCTAAGGACTTCTATCTGGAC 320

Qy   61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
Db 321 AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC 380

Qy   81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
Db 381 GCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTGCATGCCCCACATGACATGC 440

Qy 101 HisCysGlyGluGluAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu 120
Db 441 CATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG 500

Qy 121 GluProGlnAlaAlaValValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet 140
Db 501 GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATG 560

Qy 141 GluGluThrGlu 144
Db 561 GAGGAGACAGAA 572

RESULT 5
LOCUS   AR342856   926 bp   DNA   linear   PAT 17-AUG-2003
DEFINITION Sequence 1 from patent US 6576743.
ACCESSION   AR342856
VERSION   AR342856.1   GI:33738131
KEYWORDS
SOURCE   Unknown.

Left column:

```
ORGANISM   Unknown.
           Unclassified.
REFERENCE  1 (bases 1 to 926)
AUTHORS    Conklin,D.C. and Haldeman,B.A.
TITLE      Mammalian cytokine-like polypeptide-10
JOURNAL    Patent: US 6576743-A 1 10-JUN-2003;
           ZymoGenetics, Inc.; Seattle, WA
FEATURES             Location/Qualifiers
    source           1..926
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN
```

US-10-789-129-26 (1-144) x AR342856 (1-926)

```
Alignment Scores:
Pred. No.:                                   3.22e-72
Score:                        753.00         Length:        926
Percent Similarity:           100.00%        Matches:       144
Best Local Similarity:        100.00%        Conservative:    0
Query Match:                  100.00%        Mismatches:      0
                                             Indels:          0
DB:                           6              Gaps:            0
```

```
Qy     1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGACATACCGGGGCAGT 200

Qy    21 ValGlnAlaLysAspGlyAsnIleAspIleLeuArgIleLeuArgArgThrGluSerLeuGln 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   201 GTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAA 260

Qy    41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   261 GACACAAAGCCTGCGAATCGATGGCTGCCTCCTCCGGCACTTGCTAAGACTCTATCTGAC 320

Qy    61 ArgValPheLysAsnTyrGlnThrProAspHisThrTyrThrLeuArgLysIleSerSerLeu 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   321 AGGGTATTTAAAAACTACCAGACACCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC 380

Qy    81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisSerAlaHisMetThrCys 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   381 GCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTGTCATGCCCACATGACATGC 440

Qy   101 HisCysGlyGluAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   441 CATTGCTGTGGGGAGGCGATGAAGAAATACAGCACAGATTCTCACTTTGAAAAGCTG 500

Qy   141 GluGluThrGlu 144
           ||||||||||||
Db   561 GAGGAGACAGAA 572

Qy   121 GluProGlnAlaLeuAlaValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   501 GAACCTCAGGCAGCAGTGTGAAGGCTTTGGGGGAACTAGACAATTCTTCTGCAATGGATG 560

Qy   141 GluGluThrGlu 144
           ||||||||||||
Db   561 GAGGAGACAGAA 572
```

Right column:

```
TITLE      West,J., Whitmore,T.E., Yao,L., Kuechle,M.K., Dale,B.A. and
           Chandrasekher,Y.A.
           Interleukin 20: discovery, receptor identification, and role in
           epidermal function
JOURNAL    Cell 104 (1), 9-19 (2001)
PUBMED     11163236
REFERENCE  2 (bases 1 to 926)
AUTHORS    Conklin,D., Grossmann,A., Haldeman,B. and O'Hara,P.
TITLE      Homo sapiens four alpha helix cytokine allele 1
JOURNAL    Unpublished
REFERENCE  3 (bases 1 to 926)
AUTHORS    Conklin,D., Grossmann,A., Haldeman,B. and O'Hara,P.
TITLE      Direct Submission
JOURNAL    Submitted (12-JAN-2000) Biomolecular Informatics, ZymoGenetics,
           Inc., 1201 Eastlake Ave. East, Seattle, Wa. 98102, USA
FEATURES             Location/Qualifiers
    source           1..926
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /map="1q32.2"
    gene             1..926
                     /gene="ZCYTO10"
                     /allele="1"
    CDS              45..575
                     /gene="ZCYTO10"
                     /allele="1"
                     /codon_start=1
                     /product="four alpha helix cytokine"
                     /protein_id="AAF36679.1"
                     /db_xref="GI:7192207"
                     /translation="MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRN
                     GFSDIRGSVQAKDGNIDIRLRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPD
                     HYTLRKISSLANSFLTIKKDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVK
                     ALGELDILLQWMEETE"
ORIGIN
```

US-10-789-129-26 (1-144) x AF224266 (1-926)

```
Alignment Scores:
Pred. No.:                                   3.22e-72
Score:                        753.00         Length:        926
Percent Similarity:           100.00%        Matches:       144
Best Local Similarity:        100.00%        Conservative:    0
Query Match:                  100.00%        Mismatches:      0
                                             Indels:          0
DB:                           8              Gaps:            0
```

```
Qy     1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   141 TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGACATACCGGGGCAGT 200

Qy    21 ValGlnAlaLysAspGlyAsnIleAspIleLeuArgIleLeuArgArgThrGluSerLeuGln 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   201 GTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAA 260

Qy    41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   261 GACACAAAGCCTGCGAATCGATGGCTGCCTCCTCCGGCACTTGCTAAGACTCTATCTGAC 320

Qy    61 ArgValPheLysAsnTyrGlnThrProAspHisThrTyrThrLeuArgLysIleSerSerLeu 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   321 AGGGTATTTAAAAACTACCAGACACCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC 380

Qy    81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisSerAlaHisMetThrCys 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   381 GCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTGTCATGCCCACATGACATGC 440

Qy   101 HisCysGlyGluAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   441 CATTGCTGTGGGGAGGCGATGAAGAAATACAGCACAGATTCTCACTTTGAAAAGCTG 500

Qy   121 GluProGlnAlaLeuAlaValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

RESULT 6 (middle/lower left):

```
RESULT 6
AF224266
LOCUS      AF224266          926 bp    mRNA    linear   PRI 24-JAN-2001
DEFINITION Homo sapiens four alpha helix cytokine (ZCYTO10) mRNA, ZCYTO10-1
           allele, complete cds.
ACCESSION  AF224266
VERSION    AF224266.1  GI:7109206
KEYWORDS   .
SOURCE     Homo sapiens (human)
  ORGANISM Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Hominidae; Homo.
REFERENCE  1  (bases 1 to 926)
AUTHORS    Blumberg,H., Conklin,D., Xu,W.F., Grossmann,A., Brender,T.,
           Carollo,S., Eagan,M., Foster,D., Haldeman,B.A., Hammond,A.,
           Haugen,H., Jelinek,L., Kelly,J.D., Madden,K., Maurer,M.F.,
           Parrish-Novak,J., Prunkard,D., Sexson,S., Sprecher,C., Waggie,K.,
```

Db   501 GAACCTCAGGCAGCAGTTGTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATG 560

Qy   141 GluGluThrGlu 144
          ||||||||||||
Db   561 GAGGAGACGAA 572

RESULT 7

LOCUS   CS123418   462 bp   DNA   linear   PAT 16-JUL-2005
DEFINITION Sequence 18 from Patent WO2005058946.
ACCESSION   CS123418
VERSION   CS123418.1   GI:70911957
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Chan,C.
  TITLE   Methods for enhancing expression of recombinant proteins
  JOURNAL   Patent: WO 2005058946-A 18 30-JUN-2005;
            ZymoGenetics, Inc. (US)
FEATURES   Location/Qualifiers
     source   1..462
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:
Score: 749.00   Length: 462
Percent Similarity: 100.00%   Matches: 143
Best Local Similarity: 99.31%   Conservative: 1
Query Match: 99.47%   Mismatches: 0
DB: 6   Indels: 0
                                    Gaps: 0

US-10-789-129-26 (1-144) x CS123418 (1-462)

Qy   1 CysValIleAlaThrAsnLeuGlnLeuIleArgAsnGlyPheSerAspIleArgGlySer 20
          |||:|||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db   28 TGTGTGATCGCCACCAACCTGCAGGAAATCCGTAACGGTTTCTCTGAGATCCGTGGCAGC 87

Qy   21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   88 GTGCAGGCGAAAGATGGTAACATTGACATCCGTATCCTGCGTCGTACCGAGTCTCTGCAG 147

Qy   41 AspThrArgLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   148 GACACCAAAACGGCGAACCGTTGCTGCCTGCTGCGTCACCTGCTGCGTCTGTATCTGGAC 207

Qy   61 ArgValPheLysAsnTyrGlnThrProAspHisThrTyrThrLeuArgLysIleSerSerLeu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   208 CGTGTTTTCAAAAACTACCAGACCCCGGACCACTATACCCTGCGTAAAATCAGCAGCCTG 267

Qy   81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   268 GCCAACTCCTTCCTGACCATCAAAAAAGACCTGCGTCTGTGCCACGCCCACATGACCTGC 327

Qy   101 HisCysGlyTyrGluGluIleAspMetLysLysTyrSerGlnIleIleLeuSerHisPheGluLysLeu 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   328 CACTGTGGTGAGGAGAAGCAATGAAAAAATACAGCGCAGATTCTGAGCCACTTCGAAAAACTG 387

Qy   121 GluProGlnAlaAlaValValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   388 GAACCGCAGGCAGCGGTGGTGAAAGCTCTGGGTGAACTGGACATTCTGCTGCAGTGGATG 447

Qy   141 GluGluThrGlu 144
          ||||||||||||
Db   448 GAGGAGACCGAA 459

RESULT 8

LOCUS   BC069311   531 bp   mRNA   linear   PRI 06-JUL-2005
DEFINITION Homo sapiens interleukin 20, mRNA (cDNA clone MGC:96907
            IMAGE:7262116), complete cds.
ACCESSION   BC069311
VERSION   BC069311.1   GI:47480994
KEYWORDS   MGC.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 531)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE   Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2 (bases 1 to 531)
  CONSRTM   NIH MGC Project
  TITLE   Direct Submission
  JOURNAL   Submitted (29-APR-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Bethesda, MD 20892-2590, USA
  REMARK   NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT   Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Baylor Human Genome Sequencing Center
            cDNA Library Preparation: Baylor Human Genome Sequencing Center
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: amg@bcm.tmc.edu
            Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
            Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
            A.N., Gibbs, R.A.
            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRBR Plate: 1 Row: c Column: 2.
FEATURES   Location/Qualifiers
     source   1..531
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:96907 IMAGE:7262116"
                     /tissue_type="PCR rescued clones"
                     /clone_lib="NIH_MGC_244"
                     /note="Vector: pPCR-Script Amp SK(+)"
     gene   1..531
                     /gene="IL20"
                     /note="synonyms: ZCYTO10, IL10D, IL-20, MGC96907"
                     /db_xref="GeneID:50604"

ORIGIN

CDS
        /db_xref="MIM:605619"
1..531
        /gene="IL20"
        /codon_start=1
        /product="interleukin 20, precursor"
        /protein_id="AAH69311.1"
        /db_xref="GI:47480995"
        /db_xref="GeneID:50604"
        /db_xref="MIM:605619"
        /translation="MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRN
        GFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPD
        HYTLRKISSLANSFLTIKKDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVK
        ALGELDILLQWMEETE"

Alignment Scores:
Pred. No.:
Score: 749.00   4.73e-72
Percent Similarity: 100.00%   Length: 531
Best Local Similarity: 99.31%   Matches: 143
Query Match: 99.47%   Conservative: 1
DB: Mismatches: 0
                                        Indels: 0
                                        Gaps: 0
                                        8

US-10-789-129-26 (1-144) x BC069311 (1-531)

Qy   1 CysValIleAlaThrAsnLeuGlnLeuIleuArgAsnGlyPheSerAspIleArgGlySer 20
          |||||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db   97 TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGAGATACGGGCAGT 156

Qy   21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 157 GTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAA 216

Qy   41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 217 GACACAAAGCCTGCAAATCGATGCTGCCTCCTGCGACATTTGCTAAGACTCTACCTGGAC 276

Qy   61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 277 AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC 336

Qy   81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 337 GCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTGTCATGCCCACATGACATGC 396

Qy 101 HisCysGlyGluGluAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 397 CATTGTGGGGAGGAGGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG 456

Qy 121 GluProGlnAlaAlaValAlaLysSerAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet 140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 457 GAACCTCAGGCGCGCAGCAGTTGTGAAGGCTTTGGGGAACTAGACATTCTTCTGCAATGGATG 516

Qy 141 GluGluThrGlu 144
          ||||||||||||
Db 517 GAGGAGACAGAA 528

RESULT 9
BC069364

LOCUS   BC069364   531 bp   mRNA   linear   PRI 30-JUN-2004
DEFINITION Homo sapiens interleukin 20, mRNA (cDNA clone MGC:96919
            IMAGE:7262128), complete cds.
ACCESSION   BC069364
VERSION   BC069364.1 GI:47479475
KEYWORDS   MGC.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.

REFERENCE   1 (bases 1 to 531)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,

  AUTHORS   Altschul,S.F., Zeeberg,B., Bustow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE   Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2 (bases 1 to 531)
  AUTHORS   Strausberg,R.
  TITLE   Direct Submission
  JOURNAL   Submitted (29-APR-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
REMARK   NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT   Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Baylor Human Genome Sequencing Center
            cDNA Library Preparation: Baylor Human Genome Sequencing Center
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: amg@bcm.tmc.edu
            Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
            Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
            A.N., Gibbs, R.A.
            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRBR Plate: 1 Row: d Column: 2.

FEATURES   Location/Qualifiers
     source   1..531
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:96919 IMAGE:7262128"
                     /tissue_type="PCR rescued clones"
                     /clone_lib="NIH MGC_244"
                     /note="Vector: pCR-Script Amp SK(+)"
     gene   1..531
                     /gene="IL20"
                     /note="synonyms: ZCYTO10, IL10D, IL-20"
                     /db_xref="GeneID:50604"
                     /db_xref="MIM:605619"
     CDS   1..531
                     /gene="IL20"
                     /codon_start=1
                     /product="interleukin 20, precursor"
                     /protein_id="AAH69364.1"
                     /db_xref="GI:47479476"
                     /db_xref="GeneID:50604"
                     /db_xref="MIM:605619"
                     /translation="MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRN
                     GFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPD
                     HYTLRKISSLANSFLTIKKDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVK
                     ALGELDILLQWMEETE"

ORIGIN

```
Alignment Scores:
Pred. No.:                4.73e-72        Length:        531
Score:                    749.00          Matches:       143
Percent Similarity:       100.00%         Conservative:
Best Local Similarity:    99.31%          Mismatches:    1
Query Match:              99.47%          Indels:        0
DB:                       8               Gaps:          0
```

US-10-789-129-26 (1-144) x BC069364 (1-531)

```
Qy    1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
          |||||||||||||||||||||||||||||||||||||||||||::|||||||||||
Db   97 TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTCTGAGATACGGGCAGT 156

Qy   21 ValGlnHisAlaLysAspGlyAsnIleAspIleLeuArgArgThrGluSerLeuGln 40
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  157 GTGCAAGCCAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAA 216

Qy   41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  217 GACACAAAAGCCTCCGAATCGATGCTGCCTCCTCGGCCACATTTGCTAAGACTCTATCTGAC 276

Qy   61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
          ||||||||||||||||||||||||||||||||||||||||||
Db  277 AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC 336

Qy   81 AlaAsnSerPheLeuThrIleLysLysAspLeuCysHisAlaHisMetThrCys 100
          |||||||||||||||||||||||||||||||||||||||||||||
Db  337 GCCAATTCCTTTCTTACCATCAAGAAAGGACCTCGGCTTCTGCATGGCCACATGACATG 396

Qy  101 HisCysHisGlyGluGluAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu 120
          |||||||||||||||||||||||||||||||||||||||||||
Db  397 CATTGTGGGCGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGGTG 456

Qy  121 GluProGlnAlaAlaValValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet 140
          ||||||||||||||||||||||||||||||||||||||
Db  457 GAACCTCAGGCAGCAGTTGTGAAGGCCTTGGGGGAACTAGACAATTCTTCTGCAATGGATG 516

Qy  141 GluGluThrGlu 144
          ||||||||
Db  517 GAGGAGACAGAA 528
```

RESULT 10

```
BC069398
LOCUS        BC069398            531 bp    mRNA    linear    PRI 18-JUL-2005
DEFINITION   Homo sapiens interleukin 20, mRNA (cDNA clone MGC:96931
             IMAGE:7262140), complete cds.
ACCESSION    BC069398
VERSION      BC069398.1   GI:47481040
KEYWORDS     MGC.
SOURCE       Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominidae; Homo.
REFERENCE    1  (bases 1 to 531)
  AUTHORS    Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
             Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
             Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
             Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
             Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
             Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
             Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
             Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
             Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
             McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
             Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
             Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
             Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
             Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
             Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
             Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
             Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
```

```
CONSRTM     Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  CONSRTM   NIH MGC Project
  TITLE     Mammalian Gene Collection (MGC)
  JOURNAL   Direct Submission
  TITLE     Generation and initial analysis of more than 15,000 full-length
             human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  PUBMED    12477932
REFERENCE   2  (bases 1 to 531)
  AUTHORS   NIH MGC Project
  CONSRTM   NIH MGC Project
  TITLE     Direct Submission
  JOURNAL   Submitted (29-APR-2004) National Institutes of Health, Mammalian
             Gene Collection (MGC), Bethesda, MD 20892-2590, USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Baylor Human Genome Sequencing Center
             cDNA Library Preparation: Baylor Human Genome Sequencing Center
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Baylor College of Medicine Human Genome
             Sequencing Center
             Center code: BCM-HGSC
             Web site: http://www.hgsc.bcm.tmc.edu/cdna/
             Contact: amg@bcm.tmc.edu
             Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
             Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
             A.N., Gibbs, R.A.
             Clone distribution: MGC clone distribution information can be found
             through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
             Series: IRBR Plate: 1 Row: e Column: 2.
```

```
FEATURES             Location/Qualifiers
     source          1..531
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:96931 IMAGE:7262140"
                     /tissue_type="PCR rescued clones"
                     /clone_lib="NIH MGC 244"
                     /note="Vector: pPCR-Script Amp SK(+)"
     gene            1..531
                     /gene="IL20"
                     /note="synonyms: ZCYTO10, IL10D, IL-20, MGC96907"
                     /db_xref="GeneID:50604"
                     /db_xref="MIM:605619"
     CDS             1..531
                     /gene="IL20"
                     /codon_start=1
                     /product="interleukin 20, precursor"
                     /protein_id="AAH69398.1"
                     /db_xref="GI:47481041"
                     /db_xref="GeneID:50604"
                     /db_xref="MIM:605619"
                     /translation="MKASSLAFSLLSAAFVLLWTPSTGLKTLNLGSCVIATNLQEIRN
                     GFSEIRGSVQAKDGNIDIRLRRTESLQDTFPANRCCLLRHLLRLYLDRVFKNYQTPD
                     HYTLRKISSLANSFLTIKKDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVK
                     ALGELDILLQWMEETE"
```

ORIGIN

```
Alignment Scores:
Pred. No.:                4.73e-72        Length:        531
Score:                    749.00          Matches:       143
Percent Similarity:       100.00%         Conservative:
Best Local Similarity:    99.31%          Mismatches:    1
Query Match:              99.47%          Indels:        0
DB:                       8               Gaps:          0
```

US-10-789-129-26 (1-144) x BC069398 (1-531)

```
Qy    1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
          |||||||||||||||||||||||||||||||||||||||||||::|||||||||||
Db   97 TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTCTGAGATACGGGCAGT 156

Qy   21 ValGlnHisAlaLysAspGlyAsnIleAspIleLeuArgArgThrGluSerLeuGln 40
```

```
Db    157 GTGCAAGCCAAAGATGGGAAAACATTGACATCAGAAATCTTAAGGAGGACTGAGTCTTTGCAA 216
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuArgLeuTyrLeuAsp         60

Db    217 GACACAAAGCCTGGAAATCGATGTGCCTCCTCCTGCCCATTTGCTAAGACTCTATCTGGAC 276
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu   80

Db    277 AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC 336
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisSerAlaHisMetThrCys 100

Db    337 GCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTGTCATGCCCACATGACATGC 396
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    101 HisCysGlyGluGlnUalAMetLysMetLysTyrSerGlnIleIleLeuSerHisPheGluLysLeu 120

Qy    121 GluProGlnAlaAlaValAlaValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    457 GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGAACTAGACATTCTTCTGCAATGGATG 516

Qy    141 GluGluThrGlu 144
          |||||||||||
Db    517 GAGGAGACAGAA 528
```

ACCESSION BC069425

LOCUS BC069425 531 bp mRNA linear PRI 08-MAR-2005

DEFINITION Homo sapiens interleukin 20, mRNA (cDNA clone MGC:96943
     IMAGE:7262152), complete cds.

VERSION BC069425.1 GI:47479503

KEYWORDS MGC.

SOURCE Homo sapiens (human)

 ORGANISM Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
    Hominidae; Homo.

REFERENCE 1 (bases 1 to 531)

 AUTHORS Strausberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD,
     Collins FS, Wagner L, Shenmen CM, Schuler GD, Altschul SF, Zeeberg
     B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T,
     Max SI, Wang J, Hsieh F, Diatchenko L, Marusina K, Farmer AA, Rubin
     GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavant TL,
     Scheetz TE, Brownstein MJ, Usdin TB, Toshiyuki S, Carninci P,
     Prange C, Raha SS, Loquellano NA, Peters GJ, Abramson RD, Mullahy
     SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH,
     Richards S, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyk SW,
     Villalon DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahey J,
     Helton E, Ketteman M, Madan A, Rodrigues S, Sanchez A, Whiting M,
     Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakesley RW,
     Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J,
     Schmutz J, Myers RM, Butterfield YS, Krzywinski MI, Skalska U,
     Smailus DE, Schnerch A, Schein JE, Jones SJ and Marra MA.

 CONSRTM Mammalian Gene Collection Program Team

 TITLE   Generation and initial analysis of more than 15,000 full-length
     human and mouse cDNA sequences

 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

 PUBMED 12477932

REFERENCE 2 (bases 1 to 531)

 AUTHORS Direct Submission

 TITLE   Director MGC Project.

 JOURNAL Submitted (29-APR-2004) National Institutes of Health, Mammalian
     Gene Collection (MGC), Cancer Genomics Office, National Cancer
     Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
     USA

 REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov

COMMENT Contact: MGC help desk
    Email: cgapbs-r@mail.nih.gov
    Tissue Procurement: Baylor Human Genome Sequencing Center
    cDNA Library Preparation: Baylor Human Genome Sequencing Center

---

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Series: IRBR Plate: 1 Row: f Column: 2.

FEATURES   Location/Qualifiers
 source   1..531
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="MGC:96943 IMAGE:7262152"
        /tissue_type="PCR rescued clones"
        /clone_lib="NIH_MGC_244"
        /note="Vector: pPCR-Script Amp SK(+)"
 gene   1..531
        /gene="IL20"
        /note="synonyms: ZCYTO10, IL10D, IL-20, MGC96907"
        /db_xref="GeneID:50604"
        /db_xref="MIM:605619"
 CDS   1..531
        /gene="IL20"
        /codon_start=1
        /product="interleukin 20, precursor"
        /protein_id="AAH69425.1"
        /db_xref="GI:47479504"
        /db_xref="GeneID:50604"
        /db_xref="MIM:605619"
        /translation="MKASSLAPSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRN
        GFSEIRGSSVQAKDGNIDIRILRRTESLQDTKPANRCLLRHLLRLYLDRVFKNYQTPD
        HYTLRKISSLANSFLTIKKDLRLCHAHMTCHCGEBAMKKYSQILSHFEKLEPQAAVVK
        ALGELDILLQWMEETE"

ORIGIN

US-10-789-129-26 (1-144) x BC069425 (1-531)

Alignment Scores:
Pred. No.:   4.73e-72
Score: 749.00   Length: 531
Percent Similarity: 100.00%   Matches: 143
Best Local Similarity: 99.31%   Conservative: 1
Query Match: 99.47%   Mismatches: 0
DB: 8   Indels: 0
                  Gaps: 0

```
Qy      1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer  20
          ||||||||||||||||||||||||||||||||||||||||||||||||:||:||
Db      1 TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGAGATACCGGGGCAGT  60

Qy     21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln  40
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     97 GTGCAAGCCAAAGATGGGAAAACATTGACATCAGAAATCTTAAGGAGGACTGAGTCTTTGCAA 156

Qy     41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuArgLeuTyrLeuAsp  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    217 GACACAAAGCCTGGAAATCGATGTGCCTCCTCCTGCCCATTTGCTAAGACTCTATCTGGAC 276

Qy     61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu  80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    277 AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC 336

Qy     81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisSerAlaHisMetThrCys 100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    337 GCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTGTCATGCCCACATGACATGC 396

Qy    101 HisCysGlyGluGluUalAMetLysMetLysTyrSerGlnIleIleLeuSerHisPheGluLysLeu 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db      397 CATTGTGGGGAGGAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG 456
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      121 GluProGlnAlaAlaValValLysAlaLeuGlyGluLeuGlnLeuLeuGlnTrpMet 140

Db      457 GAACCTCAGCGCAGCAGTTGTGAAGGCTTTGGGGAGGAACTAGACATTCTTCTGCAATGGAATG 516
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      141 GluGluThrGlu 144

Db      517 GAGGAGACAGAA 528
                ||||||||||||
```

RESULT 12
BC069449

LOCUS   BC069449   531 bp   mRNA   linear   PRI 08-MAR-2005
DEFINITION   Homo sapiens interleukin 20, mRNA (cDNA clone MGC:96955
                IMAGE:7262164), complete cds.
ACCESSION   BC069449
VERSION   BC069449.1 GI:47480911
KEYWORDS   MGC.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Hominidae; Homo.
REFERENCE   1 (bases 1 to 531)
  AUTHORS   Strausberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD,
                Collins FS, Wagner L, Shenmen CM, Schuler GD, Altschul SF, Zeeberg
                B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T,
                Max SI, Wang J, Hsieh F, Diatchenko L, Marusina K, Farmer AA, Rubin
                GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavant TL,
                Scheetz TE, Brownstein MJ, Usdin TB, Toshiyuki S, Carninci P,
                Prange C, Raha SS, Loquellano NA, Peters GJ, Abramson RD, Mullahy
                SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH,
                Richards S, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyk SW,
                Villalon DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahey J,
                Helton E, Ketteman M, Madan A, Rodrigues S, Sanchez A, Whiting M,
                Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakesley RW,
                Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J,
                Schmutz J, Myers RM, Butterfield YS, Krzywinski MI, Skalska U,
                Smailus DE, Schnerch A, Schein JE, Jones SJ and Marra MA.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE   Generation and initial analysis of more than 15,000 full-length
                human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  PUBMED   12477932
REFERENCE   2 (bases 1 to 531)
  AUTHORS   Director MGC Project.
  TITLE   Direct Submission
  JOURNAL   Submitted (29-APR-2004) National Institutes of Health, Mammalian
                Gene Collection (MGC), Cancer Genomics Office, National Cancer
                Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                USA
REMARK   NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT   Contact: MGC help desk
                Email: cgapbs-r@mail.nih.gov
                Tissue Procurement: Baylor Human Genome Sequencing Center
                cDNA Library Preparation: Baylor Human Genome Sequencing Center
                cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                DNA Sequencing by: Baylor College of Medicine Human Genome
                Sequencing Center
                Center code: BCM-HGSC
                Web site: http://www.hgsc.bcm.tmc.edu/cdna/
                Contact: amg@bcm.tmc.edu
                Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
                Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
                A.N., Gibbs, R.A.
                Clone distribution: MGC clone distribution information can be found
                through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                Series: IRBR Plate: 1 Row: g Column: 2.
FEATURES   Location/Qualifiers
     source   1..531
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
```

```
                     /db_xref="taxon:9606"
     gene            1..531
                     /gene="IL20"
                     /note="synonyms: ZCYTO10, IL10D, IL-20, MGC96907"
                     /db_xref="GeneID:50604"
                     /db_xref="MIM:605619"
     CDS             1..531
                     /gene="IL20"
                     /clone="MGC:96955 IMAGE:7262164"
                     /tissue_type="PCR rescued clones"
                     /clone_lib="NIH_MGC_244"
                     /note="Vector: pPCR-Script Amp SK(+)"
                     /product="interleukin 20, precursor"
                     /protein_id="AAH69449.1"
                     /db_xref="GI:47480912"
                     /db_xref="GeneID:50604"
                     /db_xref="MIM:605619"
                     /translation="MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRN
                     GFSSIRGSVQAKDGNIDIRILRRTESLQDTKPANRCLLRHLLRLYLDRVFKNYQTPD
                     HYTLRKISSLANSFLTIKDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVK
                     ALGEIDILLQWMEETE"
```

ORIGIN

US-10-789-129-26 (1-144) x BC069449 (1-531)

```
Alignment Scores:
Pred. No.:              4.73e-72
Score:                  749.00              Length:            531
Percent Similarity:     100.00%             Matches:           143
Best Local Similarity:  99.31%              Conservative:        1
Query Match:            99.47%              Mismatches:          1
                        8                   Indels:              0
                                            Gaps:                0
```

```
Qy        1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerSerIleArgGlySer 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGAGATACGGCAGT 156

Qy       21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       97 GTGCAAGCCAAAGATGGAAACATTGACATAAGAATCTTAAGGAGGACTGAGTCTTTGCAA 216

Qy       41 AspThrLysProAlaAsnArgCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      217 GACACAAAAGCCTGCGAAATCGAATGCTGCCTCCTGCGGCATTTGCTAAGACTTATCTGGAC 276

Qy       61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
              |||||||||||||||||||||||||||:||||||||||||||||||:||||||||:|||
Db      277 AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC 336

Qy       81 AlaAsnSerPheLeuThrIleLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      337 GCCAATTCCTTTCTTACCATCAAGGACCTCCGGCTGTGTCATGCCCACATGACATGC 396

Qy      101 HisCysGlyGluGluAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      397 CATTGTGGGGAGGAGGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG 456

Qy      121 GluProGlnAlaAlaValValLysAlaLeuGlyGluLeuGlnLeuLeuGlnTrpMet 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      457 GAACCTCAGCGCAGCAGTTGTGAAGGCTTTGGGGAGGAACTAGACATTCTTCTGCAATGGAATG 516

Qy      141 GluGluThrGlu 144
              ||||||||||||
Db      517 GAGGAGACAGAA 528
```

RESULT 13
BC069487

LOCUS   BC069487   531 bp   mRNA   linear   PRI 08-MAR-2005
DEFINITION   Homo sapiens interleukin 20, mRNA (cDNA clone MGC:96967
                IMAGE:7262176), complete cds.
ACCESSION   BC069487
VERSION   BC069487.1 GI:47480770

```
Db      397 CATTGTGGGGAGGAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG 456
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      121 GluProGlnAlaAlaValValLysAlaLeuGlyGluLeuGlnLeuLeuGlnTrpMet 140

Db      457 GAACCTCAGCGCAGCAGTTGTGAAGGCTTTGGGGAGGAACTAGACATTCTTCTGCAATGGAATG 516
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      141 GluGluThrGlu 144

Db      517 GAGGAGACAGAA 528
                ||||||||||||
```

KEYWORDS   MGC.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominidae; Homo.
REFERENCE   1 (bases 1 to 531)
  AUTHORS   Strausberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD,
             Collins FS, Wagner L, Shenmen CM, Schuler GD, Altschul SF, Zeeberg
             B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T,
             Max SI, Wang J, Hsieh F, Diatchenko L, Marusina K, Farmer AA, Rubin
             GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavant TL,
             Scheetz TE, Brownstein MJ, Usdin TB, Toshiyuki S, Carninci P,
             Prange C, Raha SS, Loquellano NA, Peters GJ, Abramson RD, Mullahy
             SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH,
             Richards S, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyk SW,
             Villalon DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahey J,
             Helton E, Ketteman M, Madan A, Rodrigues S, Sanchez A, Whiting M,
             Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakesley RW,
             Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J,
             Schmutz J, Myers RM, Butterfield YS, Krzywinski MI, Skalska U,
             Smailus DE, Schnerch A, Schein JE, Jones SJ and Marra MA.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE   Generation and initial analysis of more than 15,000 full-length
             human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2 (bases 1 to 531)
  AUTHORS   Direct Submission
  TITLE   Director MGC Project.
  JOURNAL   Submitted (29-APR-2004) National Institutes of Health, Mammalian
             Gene Collection (MGC), Cancer Genomics Office, National Cancer
             Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
             USA
  REMARK   NIH-MGC Project URL: http://mgc.nci.nih.gov
  COMMENT   Contact: MGC help desk
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Baylor Human Genome Sequencing Center
             cDNA Library Preparation: Baylor Human Genome Sequencing Center
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Baylor College of Medicine Human Genome
             Sequencing Center
             Center code: BCM-HGSC
             Web site: http://www.hgsc.bcm.tmc.edu/cdna/
             Contact: amg@bcm.tmc.edu
             Gunaratne, P.H., Garcia, A.M, Lu, X., Hulyk, S.W., Loulseged, H.,
             Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
             A.N., Gibbs, R.A.
             clone distribution: MGC clone distribution information can be found
             through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
             Series: IRBR Plate: 1 Row: h Column: 2.
FEATURES   Location/Qualifiers
     source   1..531
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:96967 IMAGE:7262176"
                     /tissue_type="PCR rescued clones"
                     /clone_lib="NIH MGC 244"
                     /note="Vector: pPCR-Script Amp SK(+)"
     gene   1..531
                     /gene="IL20"
                     /gene="IL20"
                     /note="synonyms: ZCYTO10, IL10D, IL-20, MGC96907"
                     /db_xref="GeneID:50604"
                     /db_xref="MIM:605619"
     CDS   1..531
                     /gene="IL20"
                     /codon_start=1
                     /product="interleukin 20, precursor"
                     /protein_id="AAH69487.1"
                     /db_xref="GI:47480771"
                     /db_xref="MIM:605619"
                     /db_xref="GeneID:50604"

ORIGIN
             /db_xref="MIM:605619"
             /translation="MKASSLAFSLLSAAFYLLWTPSTGLKTLNIGSCVIATNLQEIRN
             GFSEIRGSVQAKDGNIDIRILRRTESLQDTVKRPANRCLLRHLLRRLYLDRVFKNYQTPD
             HYTLRKISSLANSFLTIKKDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVK
             ALGELDILLQWMEETE"

US-10-789-129-26 (1-144) x BC069487 (1-531)

Alignment Scores:
Pred. No. :   4.73e-72   Length: 531
Score: 749.00   Matches: 143
Percent Similarity: 100.00%   Conservative: 1
Best Local Similarity: 99.31% Mismatches: 0
Query Match: 99.47%   Indels: 0
DB: 8   Gaps: 0

Qy   1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
          ||||||||||||||||||||||||||||||||||||||||||||||||::|||||||||||
Db   1 TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCGAGATATACGGGGCAGT 60

Qy   21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAA 156

Qy   41 AspThrLysProAlaAsnArgCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   157 GACACAAAAGCCTGCAAATCGATGCTGCCCTCCTGGGCCATTTGCTAAGACTCTATCTGGAC 276

Qy   61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   277 AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC 336

Qy   81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   337 GCCAATTCCTTCCTTACCATCAAGAAGGACCTCCGGCTCTGTCATGCCCACATGACATGC 396

Qy   101 HisCysGlyGluGluAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   397 CATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG 456

Qy   121 GluProGlnAlaAlaValValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet 140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   457 GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGTGAACTAGACATTCTTCTGCAATGGATG 516

Qy   141 GluGluThrGlu 144
          ||||||||||||
Db   517 GAGGAGACAGAA 528

RESULT 14
BC069523
BC069523
LOCUS   BC069523   531 bp   mRNA   linear   PRI 08-MAR-2005
DEFINITION   Homo sapiens interleukin 20, mRNA (cDNA clone MGC:96884
             IMAGE:7262093), complete cds.
ACCESSION   BC069523
VERSION   BC069523.1 GI:47479431
KEYWORDS   MGC.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominidae; Homo.
REFERENCE   1 (bases 1 to 531)
  AUTHORS   Strausberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD,
             Collins FS, Wagner L, Shenmen CM, Schuler GD, Altschul SF, Zeeberg
             B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T,
             Max SI, Wang J, Hsieh F, Diatchenko L, Marusina K, Farmer AA, Rubin
             GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavant TL,
             Scheetz TE, Brownstein MJ, Usdin TB, Toshiyuki S, Carninci P,
             Prange C, Raha SS, Loquellano NA, Peters GJ, Abramson RD, Mullahy
             SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH,
             Richards S, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyk SW,
             Villalon DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahey J,

Left column

```
          Helton E, Ketteman M, Madan A, Rodrigues S, Sanchez A, Whiting M,
          Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakesley RW,
          Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J,
          Schmutz J, Myers RM, Butterfield YS, Krzywinski MI, Skalska U,
          Smailus DE, Schnerch A, Schein JE, Jones SJ and Marra MA.
  CONSRTM Mammalian Gene Collection Program Team
  TITLE   Generation and initial analysis of more than 15,000 full-length
          human and mouse cDNA sequences
  JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED 12477932
REFERENCE 2 (bases 1 to 531)
  CONSRTM Director MGC Project.
  TITLE   Direct Submission
  JOURNAL Submitted (29-APR-2004) National Institutes of Health, Mammalian
          Gene Collection (MGC), Cancer Genomics Office, National Cancer
          Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
          USA
  REMARK  NIH-MGC Project URL: http://mgc.nci.nih.gov
  COMMENT Contact: MGC help desk
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Baylor Human Genome Sequencing Center
          cDNA Library Preparation: Baylor Human Genome Sequencing Center
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Baylor College of Medicine Human Genome
          Sequencing Center
          Center code: BCM-HGSC
          Web site: http://www.hgsc.bcm.tmc.edu/cdna/
          Contact: amg@bcm.tmc.edu
          Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
          Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
          A.N., Gibbs, R.A.
          Clone distribution: MGC clone distribution information can be found
          through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
          Series: IRBP Plate: 1 Row: a Column: 3.
FEATURES             Location/Qualifiers
     source          1..531
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:96884 IMAGE:7262093"
                     /tissue_type="PCR rescued clones"
                     /clone_lib="NIH_MGC_244"
                     /note="Vector: pPCR-Script Amp SK(+)"
     gene            1..531
                     /gene="IL20"
                     /note="synonyms: ZCYTO10, IL10D, IL-20, MGC96907"
                     /db_xref="GeneID:50604"
                     /db_xref="MIM:605619"
     CDS             1..531
                     /gene="IL20"
                     /codon_start=1
                     /product="interleukin 20, precursor"
                     /protein_id="AAH69523.1"
                     /db_xref="GI:47479432"
                     /db_xref="GeneID:50604"
                     /db_xref="MIM:605619"
                     /translation="MKASSLAFSLLSAAFYLLWTPSTGLKTNLNLGSCVIATNLQEIRN
                     GFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCLLRHLLRLYLDRVFKNYQTPD
                     HYTLRKISSLANSFLTIKKDLRLCHAHMTCHGEEAMKKYSQILSHFEKLEPQAAVVK
                     ALGELDILLQWMEETS"
ORIGIN
```

```
US-10-789-129-26 (1-144) x BC069523 (1-531)

Alignment Scores:
Pred. No.:                 1
Pred:                      4.73e-72
Score:                     749.00        Length:        531
Percent Similarity:        100.00%       Matches:       143
Best Local Similarity:     99.31%        Conservative:  1
Query Match:               99.47%        Mismatches:    0
DB:                        8             Indels:        0
                                         Gaps:          0
```

Right column

```
RESULT 15
BC069559
LOCUS       BC069559                 531 bp    mRNA    linear   PRI 08-MAR-2005
DEFINITION  Homo sapiens interleukin 20, mRNA (cDNA clone MGC:96896
            IMAGE:7262105), complete cds.
ACCESSION   BC069559
VERSION     BC069559.1  GI:47480991
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 531)
  AUTHORS   Strausberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD,
            Collins FS, Wagner L, Shenmen CM, Schuler GD, Altschul SF, Zeeberg
            B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T,
            Max SI, Wang J, Hsieh F, Diatchenko L, Marusina K, Farmer AA, Rubin
            GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavant TL,
            Scheetz TE, Brownstein MJ, Usdin TB, Toshiyuki S, Carninci P,
            Prange C, Raha SS, Loquellano NA, Peters GJ, Abramson RD, Mullahy
            SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH,
            Richards S, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyk SW,
            Villalon DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahey J,
            Helton E, Ketteman M, Madan A, Rodrigues S, Sanchez A, Whiting M,
            Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakesley RW,
            Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J,
            Schmutz J, Myers RM, Butterfield YS, Krzywinski MI, Skalska U,
            Smailus DE, Schnerch A, Schein JE, Jones SJ and Marra MA.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2 (bases 1 to 531)
  CONSRTM   Director MGC Project.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-APR-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
```

```
Qy    1  CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer   20
         |||||||||||||||||||||||||||||||||||||||||||::||||||||||||||
Db   97  TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGGATTTTCTGAGATACGGGGCAGT  156

Qy   21  ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln   40
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  157  GTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAA  216

Qy   41  AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  217  GACACAAAGCCTGCAAATCGATGCTGCCTCCTGCGCCATTTGCTTAGACTCTATCTGGAC  276

Qy   61  ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu   80
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  277  AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC  336

Qy   81  AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys  100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  337  GCCAATTCTTTCTTACCATCAAGAAGGACCTCCGGCTGTGTCATGCCCACATGACATGC  396

Qy  101  HisCysGlyGluGluAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  397  CATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG  456

Qy  121  GluProGlnAlaAlaValValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet  140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  457  GAACCTCAGGCAGCAGTTGTTGAAGGCCTTTGGGGAACTAGACATTCTTCTGCAATGGATG  516

Qy  141  GluGluThrGlu  144
         ||||||||||||
Db  517  GAGGAGACAGAA  528
```

REMARK   NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT   Contact: MGC help desk
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Baylor Human Genome Sequencing Center
          cDNA Library Preparation: Baylor Human Genome Sequencing Center
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Baylor College of Medicine Human Genome
          Sequencing Center
          Center code: BCM-HGSC
          Web site: http://www.hgsc.bcm.tmc.edu/cdna/
          Contact: amg@bcm.tmc.edu
          Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
          Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
          A.N., Gibbs, R.A.

          Clone distribution: MGC clone distribution information can be found
          through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
          Series: IRBB Plate: 1 Row: b Column: 3.

FEATURES   Location/Qualifiers
     source   1..531
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:96896 IMAGE:7262105"
                     /tissue_type="PCR rescued clones"
                     /clone_lib="NIH MGC_244"
                     /note="Vector: pPCR-Script Amp SK(+)"
                     1..531
     gene   1..531
                     /gene="IL20"
                     /note="synonyms: ZCYTO10, IL10D, IL-20, MGC96907"
                     /db_xref="GeneID:50604"
                     /db_xref="MIM:605619"
     CDS   1..531
                     /gene="IL20"
                     /codon_start=1
                     /product="interleukin 20, precursor"
                     /protein_id="AAH69559.1"
                     /db_xref="GI:47480992"
                     /db_xref="GeneID:50604"
                     /db_xref="MIM:605619"
                     /translation="MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRN
                     GFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPD
                     HYTLRKISSLANSFLTIKKDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVK
                     ALGELDILLQWMEETE"

ORIGIN

Alignment Scores:
Pred. No.:   1
Score: 4.73e-72
Score: 749.00   Length: 531
Percent Similarity: 100.00%   Matches: 143
Best Local Similarity: 99.31%   Conservative: 1
Query Match: 99.47%   Mismatches: 1
DB: 8   Indels: 0
                                          Gaps: 0

US-10-789-129-26 (1-144) x BC069559 (1-531)

Qy   1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   97 TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGAGATACGGGGCAGT 156

Qy   21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   157 GTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAA 216

Qy   41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   217 GACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTCAGACTCTATCTGGAC 276

Qy   61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   277 AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAAGACAGCAGCCTC 336

Qy   81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 28, 2005, 12:45:53 ; Search time 496 Seconds
                                          (without alignments)
                                         1934.911 Million cell updates/sec

Title: US-10-789-129-26
Perfect score: 753
Sequence: 1 CVIAINLQEIRNGFSDIRGS..........AVVKALGELDILLQWMEETE 144

Scoring table: BLOSUM62
            Xgapop 10.0 , Xgapext 0.5
            Ygapop 10.0 , Ygapext 0.5
            Fgapop 6.0 , Fgapext 7.0
            Delop   6.0 , Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/ccp2_1/USPTO_spool_p/US10789129/runat_23122005_152719_20254/app_query.fasta_1.327
-DB=N_Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10789129 @CGN 1.1 1096 @runat_23122005_152719 20254 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -THREADS=1 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_21:*
            1: geneseqn1980s:*
            2: geneseqn1990s:*
            3: geneseqn2000s:*
            4: geneseqn2001as:*
            5: geneseqn2001bs:*
            6: geneseqn2002as:*
            7: geneseqn2002bs:*
            8: geneseqn2003as:*
            9: geneseqn2003bs:*
           10: geneseqn2003cs:*
           11: geneseqn2004as:*
           12: geneseqn2004ds:*
           13: geneseqn2004bs:*
           14: geneseqn2005s:*

                            SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Match	Query Length	DB	ID	Description
1	753	100.0	528	12	ADM95042	Adm95042 Human Int
2	753	100.0	531	14	ADV42800	Adv42800 Human psy
3	753	100.0	926	2	AAX77692	Aax77692 Human Zcy
4	753	100.0	926	9	ACF05161	Acf05161 Polynucle
5	753	100.0	926	10	AAD61821	Aad61821 Human cyt
6	753	100.0	926	10	ADG46668	Adg46668 Human Zcy
7	753	100.0	926	12	ADQ88066	Adq88066 Human Zcy
8	753	100.0	926	13	ADR16327	Adr16327 Human cyt
9	753	100.0	926	13	ADR24325	Adr24325 Breast ca
10	753	100.0	926	13	ADS18362	Ads18362 Human Zcy
11	753	100.0	926	14	AEA50048	Aea50048 Full leng
12	753	100.0	926	14	AEA28786	Aea28786 Human int
13	749	99.5	462	8	AEB26649	Aeb26649 Human int
14	749	99.5	462	8	ABV75151	Abv75151 Human int
15	749	99.5	513	8	ABV75154	Abv75154 EC sequen
16	749	99.5	528	12	ADL15289	Adl15289 Human int
17	749	99.5	867	6	ABQ74562	Abq74562 Human LP8
18	749	99.5	867	6	ABV73092	Abv73092 Human LP8
19	749	99.5	925	12	ADN12153	Adn12153 Interleuk
20	746	99.1	926	13	ADS31716	Ads31716 DNA encod
21	746	99.1	926	13	ADS92718	Ads92718 DNA encod
22	739	98.1	462	3	AAA37138	Aaa37138 Human PRO
23	739	98.1	1571	4	AAF54484	Aaf54484 Primer #1
24	739	98.1	1571	4	AAS21292	Aas21292 Human cDN
25	739	98.1	1571	4	AAS21516	Aas21516 Human cDN
26	739	98.1	1571	4	AAS46229	Aas46229 Human DNA
27	739	98.1	1571	6	AAF92126	Aaf92126 Human PRO
28	739	98.1	1571	6	ABK33644	Abk33644 cDNA enco
29	739	98.1	1571	6	ABS74446	Abs74446 Human CDN
30	739	98.1	1571	6	ABL88214	Abl88214 Human ang
31	739	98.1	1571	6	ABL95703	Abl95703 Human PRO
32	739	98.1	1571	7	ADY31957	Ady31957 Novel hum
33	739	98.1	1571	8	ACA89679	Aca89679 cDNA enco
34	739	98.1	1571	8	ACA73689	Aca73689 Human sec
35	739	98.1	1571	8	ACA06004	Aca06004 Human sec
36	739	98.1	1571	8	ACA66838	Aca66838 cDNA enco
37	739	98.1	1571	8	ACA91232	Aca91232 Novel hum
38	739	98.1	1571	8	ACD81609	Acd81609 Human CDN
39	739	98.1	1571	8	ACF20413	Acf20413 Human sec
40	739	98.1	1571	8	ACF19799	Acf19799 Human sec
41	739	98.1	1571	8	ACD22087	Acd22087 Human sec
42	739	98.1	1571	8	ACF13252	Acf13252 Human sec
43	739	98.1	1571	8	ACD25355	Acd25355 Human sec
44	739	98.1	1571	8	ACF00404	Acf00404 Human sec
45	739	98.1	1571	8	ACA60431	Aca60431 Novel hum

                            ALIGNMENTS

RESULT 1
ADM95042

ID   ADM95042 standard; DNA; 528 BP.
XX
AC   ADM95042;
XX
DT   17-JUN-2004 (first entry)
XX
DE   Human Interleukin-20 (IL-20) gene SeqID4.
XX
KW   colon cancer; interleukin 20 receptor alpha chain;
KW   IL-20 receptor alpha chain; cytostatic; gene; ds; human.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FH
FT   CDS   1..528
FT   /*tag= a
FT   /product= "Human Interleukin-20 (IL-20) protein"
FT   /partial
FT   /note= "No stop codon"
XX
PN   JP2004075569-A.
XX
PD   11-MAR-2004.
XX
PF   12-AUG-2002; 2002JP-00234880.

PR   12-AUG-2002; 2002JP-00234880.
XX
PA   (TAKE) TAKEDA CHEM IND LTD.
XX
DR   WPI; 2004-320878/30.
DR   P-PSDB; ADM95041.
XX
PT   Agent useful for prevention and/or treatment of colon cancer, comprises
PT   interleukin 20 (IL-20), IL-20 receptor alpha chain, IL-20 receptor beta
     chain.
XX
PS   Disclosure; SEQ ID NO 10; 50pp; Japanese.
XX
CC   This invention relates to a novel agent for prevention and/or treatment
CC   of colon cancer, comprising of the interleukin 20 (IL-20) receptor alpha
CC   chain, its partial peptide or salt. The invention may be useful for the
CC   development of compounds with a cytostatic activity. A diagnostic agent is
CC   useful for diagnosis of colon cancer. By using IL-20, IL-20 receptor, its
CC   salt or its peptide, compounds that have altered binding property towards
CC   them can be efficiently screened. The present sequence is that of a gene
CC   which encodes the human Interleukin-20 protein and which is related to
CC   the invention.
XX
SQ   Sequence 528 BP; 148 A; 129 C; 122 G; 129 T; 0 U; 0 Other;
XX

Alignment Scores:
Pred. No.:
Score: 5.13e-87   Length: 528
Percent Similarity: 753.00   Matches: 144
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
                         12   Indels: 0
                                         Gaps: 0

US-10-789-129-26 (1-144) x ADM95042 (1-528)

Qy   1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   97 TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCGACATACGGGGCAGT 156

Qy   21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 157 GTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAA 216

Qy   41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 217 GACACAAAAGCCTGCAAATCGATGTGCCTCCTGCGGCCATTTGCTAAGACTTCTATCTGGAC 276

Qy   61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgGlyIleSerSerLeu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 277 AGGGTTATTTAAAAACTACCAGAACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC 336

Qy   81 AlaAsnSerPheLeuThrIleLeuTyrGlyArgLeuCysHisAlaHisMetThrCys 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 337 GCCAATTCCTTTCTTTACCATCAAGAAGGAGACTCCGGCGCTCTGCTCATCGCTGC 396

Qy 101 HisCysGlyGlyGlnAlaMetLysLysTyrSerGlnIleLeuSerHisPheGlyLysLeu 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 397 CATTGTGGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAACTG 456

Qy 121 GluProGlnAlaAlaValValLysAspIleLeuGluAspLeuLeuGlnTrpMet 140
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 457 GAACCTCAGCCAGCAGTTGTGAAGGACATTCTTGCAATGGATG 516

Qy 141 GluGluThrGlu 144
          |||||||||||
Db 517 GAGGAGACAGAA 528

XX
DT   10-MAR-2005 (first entry)
XX
DE   Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 428.
XX
KW   microarray; psychoneuroendocrinimmune; chronic fatigue;
KW   non-insulin dependent diabetes; allergy; immune disorder; inflammation;
KW   cancer; neoplasm; infection; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200410899-A2.
XX
PD   16-DEC-2004.
XX
PF   04-JUN-2004; 2004WO-US017686.
XX
PR   04-JUN-2003; 2003US-04759915P.
XX
PA   (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Nicholson A, Vernon SD;
XX
DR   WPI; 2005-031682/03.
XX
PT   New microarray comprising probes for genes involved in
PT   psychoneuroendocrinimmune (PNI) activity, useful in diagnosing a
PT   condition associated with PNI activity, e.g. inflammatory or infectious
PT   diseases.
XX
PS   Claim 1; SEQ ID NO 428; 254pp; English.
XX
CC   The invention relates to a new microarray which comprises probes for
CC   genes involved in psychoneuroendocrinimmune (PNI) activity. The
CC   microarray is useful in diagnosing a condition associated with PNI
CC   activity, such as CFS, type-2 diabetes, allergic condition, inflammation,
CC   cancer and infection. The present sequence represents a
CC   psychoneuroendocrinimmune gene expressed sequence tag. Note the
CC   specificatio mentions SEQ ID NO of up to 3314 but only sequences up to
CC   SEQ ID NO 1829 are provided.
XX
SQ   Sequence 531 BP; 149 A; 129 C; 123 G; 130 T; 0 U; 0 Other;
XX

Alignment Scores:
Pred. No.:
Score: 5.18e-87   Length: 531
Percent Similarity: 753.00   Matches: 144
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
                         14   Indels: 0
                                         Gaps: 0

US-10-789-129-26 (1-144) x ADV42800 (1-531)

Qy   1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   97 TGTGTGATCGGCCACAAACCTTCAGGAAATACGAAATGGATTTTCGACATACGGGGCAGT 156

Qy   21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 157 GTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAA 216

Qy   41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 217 GACACAAAAGCCTGCAAATCGATGTGCCTCCTGCGGCCATTTGCTAAGACTTCTATCTGGAC 276

Qy   61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgGlyIleSerSerLeu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 277 AGGGTTATTTAAAAACTACCAGAACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC 336

Qy   81 AlaAsnSerPheLeuThrIleLeuTyrGlyArgLeuCysHisAlaHisMetThrCys 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 337 GCCAATTCCTTTCTTTACCATCAAGAAGGAGACTCCGGCGCTCTGCTCATCGCTGC 396

RESULT 2
ID   ADV42800 standard; cDNA; 531 BP.
XX
AC   ADV42800;

```
Qy    101  HisCysGlyGluGluAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu  120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    397  CATTGTGGGGAGGAGGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG  456

Qy    121  GluProGlnAlaAlaValValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet  140
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    457  GAACCTCAGGCAGCAGGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATG  516

Qy    141  GluGluThrGlu  144
           ||||||||||||
Db    517  GAGGAGACAGAA  528
```

```
RESULT 3
AAX77692
XX
ID   AAX77692 standard; cDNA; 926 BP.
XX
AC   AAX77692;
XX
DT   09-AUG-1999  (first entry)
XX
DE   Human Zcyto10 allele 1 cDNA.
XX
KW   Zcyto10; four alpha helix cytokine; vulnerary; cytostatic; haemostatic;
KW   anti-inflammatory; anti-asthmatic; growth factor; maintenance factor;
KW   trachea; salivary gland; stomach; pancreas; muscle; gene therapy; cancer;
KW   proliferation; differentiation; modulator; gastrointestinal tract;
KW   oral cavity; asthma; tracheobronchial tract; bronchitis; wound healing;
KW   platelet count; thrombocytopenia; human; ss.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             45..575
FT                   /*tag= a
FT                   /product= "Zcyto10"
XX
PN   WO9927103-A1.
XX
PD   03-JUN-1999.
XX
PF   25-NOV-1998; 98WO-US025228.
XX
PR   26-NOV-1997; 97US-0979156.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Conklin DC, Haldeman BA, Grossmann A;
XX
DR   WPI; 1999-357840/30.
DR   P-PSDB; AAY08661.
XX
PT   New mammalian cytokine-like polynucleotide useful in the treatment of
PT   asthma and bronchitis.
XX
PS   Claim 3; Page 63-64; 82pp; English.
XX

CC   This invention describes a novel mammalian four alpha helix cytokine
CC   designated Zcyto10 which has vulnerary, cytostatic, anti-inflammatory,
CC   anti-asthmatic and haemostatic activity. Zcyto10 may be a growth and/or
CC   maintenance factor in the trachea and salivary glands, stomach, pancreas
CC   and muscle. Zcyto10 polynucleotides are useful as sources of primers and
CC   probes, and to determine if the Zcyto10 gene is present on chromosome 1,
CC   or to detect any mutations that may have occurred. Zcyto10
CC   polynucleotides are also useful as gene therapy reagents. The Zcyto10
CC   polypeptide, its fragments, and antibodies, as well as compounds
CC   identified as having binding affinity to Zcyto10, should be useful in the
CC   treatment of conditions associated with abnormal physiology or
CC   development, including abnormal proliferation, e.g. cancerous conditions,
CC   or degenerative conditions or altered immunity.The products are also
CC   useful for modulating cell proliferation, cell differentiation or
CC   cytokine production in the prevention or treatment of conditions
CC   characterized by abnormal cell proliferation, cell differentiation or
CC   cytokine production. Zcyto10 polypeptides, agonists and antagonists may
```

```
CC   be therapeutically useful in the regeneration of the gastrointestinal
CC   tract or oral cavity, as well as in the treatment of asthma, and other
CC   diseases of the tracheobronchial tract such as bronchitis. Zcyto10
CC   polypeptides may also be useful to promote wound healing, and to increase
CC   platelet count, e.g. in cancer patients who experience thrombocytopenia
CC   due to chemotherapy or radiation therapy
XX
SQ   Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;
```

```
Alignment Scores:
Pred. No.:                 1.17e-86      Length:         926
Score:                     753.00        Matches:        144
Percent Similarity:        100.00%       Conservative:   0
Best Local Similarity:     100.00%       Mismatches:     0
Query Match:               100.00%       Indels:         0
DB:                        2             Gaps:           0

US-10-789-129-26 (1-144) x AAX77692 (1-926)

Qy      1  CysValIleAlaThrAsnLeuGlnGluIleIleArgAsnGlyPheSerAspIleArgGlySer   20
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    141  TGTGTTGATCGCCACAAACCTTCAGGAAATACGAAAATGGATTTTCTGACATACGGGGCAGT  200

Qy     21  ValGlnAlaLysAspGlyAsnIleAspAspIleArgIleLeuArgArgThrGluSerLeuGln   40
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    201  GTGCAAGCCAAAGATGGAAACATTGACGATATCAGGATTCTTAGGAGGACTGAGTCTTTGCAA  260

Qy     41  AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp   60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    261  GACACAAAGCCTGCAAATCGATGCTGCCTCCTGCGCCATTGCTAAGACTCTATCTGGAC  320

Qy     61  ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysLeuSerSerLeu   80
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    321  AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC  380

Qy     81  AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys  100
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    381  GCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTGTCATGCCCACATGACATGC  440

Qy    101  HisCysGlyGluGluAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu  120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    441  CATTGTGGGGAGGAGGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG  500

Qy    121  GluProGlnAlaAlaValValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet  140
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    501  GAACCTCAGGCAGCAGGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATG  560

Qy    141  GluGluThrGlu  144
           ||||||||||||
Db    561  GAGGAGACAGAA  572
```

```
RESULT 4
ACF05161
XX
AC   ACF05161;
XX
ID   ACF05161 standard; cDNA; 926 BP.
XX
DT   06-NOV-2003  (first entry)
XX
DE   Polynucleotide encoding human interleukin-20.
XX
KW   Human; interleukin-20; IL-20; cervical cancer; cytostatic; virucide;
KW   gene; ss.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             45..575
FT                   /*tag= a
FT                   /product= "Human IL-20"
FT   sig_peptide     45..116
FT                   /*tag= b
FT   mat_peptide     117..572
```

/*tag= c

```
FT
XX
PN   WO2003051384-A1.
XX
PD   26-JUN-2003.
XX
PF   17-DEC-2002; 2002WO-US040309.
XX
PR   17-DEC-2001; 2001US-0341783P.
XX
PA   (LUNN/) LUNN P G.
PA
PI   Chandrasekher YA, McKernan PA;
XX
DR   WPI; 2003-569114/53.
DR   P-PSDB; ABR62464.
XX
PT   Inhibiting the growth and/or proliferation of cervical cancer cells,
PT   useful for treating cervical cancer or human papilloma virus infection,
PT   comprises bringing Interleukin-20 (Il-20) into contact with the cervical
PT   cancer cells.
XX
PS   Disclosure; Page 11-12; 26pp; English.
XX
CC   The present sequence is that of a polynucleotide encoding human
CC   interleukin-20 (IL-20), including the signal sequence. The invention
CC   relates to the use of IL-20 for treating cervical cancer or cells
CC   infected with human papilloma virus. IL-20 can be administered alone or
CC   in conjunction with radiation or chemotherapeutic agents or surgical
CC   excision of the involved cells or lesions
XX
SQ   Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;

US-10-789-129-26 (1-144) x ACF05161 (1-926)

Alignment Scores:
Pred. No.:
Score:                    1.17e-86
Percent Similarity:       100.00%      Length:         926
Percent Similarity:       100.00%      Matches:        144
Best Local Similarity:    100.00%      Conservative:   0
Query Match:              9            Mismatches:     0
                                       Indels:         0
DB:                                    Gaps:           0

  1 CysValIleAlaThrAsnLeuGlnGluIleArgAlaAsnGlyPheSerAspIleArgGlySer 20
141 TGCGTGATCGCCACAAACCTTCAGGAAAATACGAAATGGATTTTCTGACATACGGGGCAGT 200
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    TGCGTGATCGCCACAAACCTTCAGGAAAATACGAAATGGATTTTCTGACATACGGGGCAGT 200

 21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
201 GTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAA 260

 41 AspThrLysProAlaAsnArgCysLeuLeuUArgHisLeuLeuArgLeuTyrLeuAsp 60
261 GACACAAAGCCTGCGAATCGATGCGTCCTCCTGCCCATTTGCTAAGACTTCTATCTGGAC 320

 61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
321 AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC 380

 81 AlaAsnSerPheLeuThrIleLeuLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
381 GCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTGTCATGCCCACATGACATGC 440

101 HisCysGlyGlyUGlnUalaMetLeuGlyLysTyrSerGlnIleLeuSerHisPheGlyLysLeu 120
441 CATTGTGGGGAGGGAGCAAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG 500

121 GluProGlnAlaAlaValAlaValLysSerAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet 140
501 GAACCTCAGGCAGCAGTTGTGAAGGGCTTTGGGGAGAACTAGACAGATTTCTTCCAATGGATG 560

141 GluGluThrGlu 144
    ||||||||||||
```

```
Db       561 GAGGAGACAGAA 572

RESULT 5
AAD61821
ID   AAD61821 standard; cDNA; 926 BP.
XX
AC   AAD61821;
XX
DT   15-JAN-2004 (first entry)
XX
DE   Human cytokine-like polypeptide-10 (Zcyto10) cDNA.
XX
OS   Homo sapiens.
XX
KW   Human; cytokine-like polypeptide-10; Zcyto10; therapy; thrombocytopaenia;
KW   autoimmune disease; insulin-dependent diabetes mellitus; immune response;
KW   rheumatoid arthritis; multiple sclerosis; infection; radiation therapy;
KW   asthma; bronchitis; wound healing; periodontal disease; antiinflammatory;
KW   psoriasis; eczema; dry skin; oral cavity; muscle atrophy; haemostatic;
KW   cancer; vulnerary; chromosome 1; gene; ss.
XX
FH   Key             Location/Qualifiers
FT   CDS             45..575
FT                   /tag= a
FT                   /product= "Human Zcyto10"
FT   sig_peptide     45..116
FT                   /tag= b
FT   mat_peptide     117..572
FT                   /tag= c
FT                   /product= "Mature human Zcyto10"
XX
PN   US6576743-B1.
XX
PI   Conklin DC, Haldeman BA;
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PD   10-JUN-2003.
XX
DR   WPI; 2003-799828/75.
DR   P-PSDB; ABW00889.
XX
PF   17-MAY-1999; 99US-00313458.
XX
PR   26-NOV-1997; 97US-0065997P.
PR   25-NOV-1998; 98US-00199586.
XX
PT   Novel human cytokine-like polypeptide-10, Zcyto10, useful for treating
PT   insulin-dependent diabetes mellitus, rheumatoid arthritis, multiple
PT   sclerosis, asthma, psoriasis and inhibiting cancer cell growth.
XX
PS   Disclosure; Col 29-30; 0pp; English.
XX
CC   The invention relates to an isolated human cytokine-like polypeptide-10
CC   (Zcyto10) polypeptide. Zcyto10 is useful for prevention or treatment of
CC   conditions characterised by improper cell proliferation, cell
CC   differentiation or cytokine production. Zcyto10 is useful for treating
CC   autoimmune diseases such as insulin-dependent diabetes mellitus,
CC   rheumatoid arthritis, multiple sclerosis, etc., by inhibiting cellular
CC   immune response. The invention is useful for inhibiting cancer cell
CC   growth or proliferation, for stimulating immune system to combat
CC   microbial or viral infections, for increasing platelet production, and
CC   thus useful in cancer patients who experience thrombocytopaenia due to
CC   cancer therapy or radiation therapy. Zcyto10 is useful in trachea-
CC   specific or tracheobronchial-specific applications, such as in the
CC   maintenance or would repair of the tracheobronchial epithelium or cells
CC   underlying the same, in regulating mucous production or mucociliary
CC   clearance of debris or in treatment of asthma, bronchitis or other
CC   diseases of the tracheobronchial tract. Zcyto10 may also enhance wound
CC   healing and promote regeneration of affected tissues which may be
CC   especially useful in the treatment of periodontal disease. Zcyto10 can be
CC   used to treat skin conditions such as psoriasis, eczema and dry skin in
CC   general. Zcyto10 is useful for regenerating gastrointestinal tract or
```

```
CC   oral cavity and for modulating muscle tone in the tracheobronchial tract,
CC   and for treating muscle atrophy in the elderly, sick or bed-ridden.
CC   Zcyto10 is also useful for promoting wound healing. The present sequence
CC   is human Zcyto10 cDNA. The Zcyto10 gene is located on chromosome 10
XX
SQ   Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;
```

```
Alignment Scores:
Pred. No.:
Score:                    1.17e-86     Length:         926
Percent Similarity:       753.00       Matches:        144
Best Local Similarity:    100.00%      Conservative:   0
Query Match:              100.00%      Mismatches:     0
DB:                       10           Indels:         0
                                       Gaps:           0

US-10-789-129-26 (1-144) x AAD61821 (1-926)

Qy    1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  141 TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCGACATACGGGGCAGT 200

Qy   21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgThrGluSerLeuGln 40
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  201 GTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGACTGAGTCTTTGCAA 260

Qy   41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  261 GACACAAAGCCTGCAAATCGATGCTGCCTCCTGCGCCATTTGCTTAAGACTCTACTGGAC 320

Qy   61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  321 AGGGTATTTAAAAACTACCAGACACCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC 380

Qy   81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisSerAlaHisMetThrCys 100
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  381 GCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTGTCCATGCCCACACATGACATGC 440

Qy  101 HisCysGlyGluGlyUlaMetLysTyrSerGlnIleLeuSerHisPheGluLysLeu 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  441 CATTGTGGGGAGGGAAGCAATGAAGAAATACAGCCAGATTCTGAGCTCACTTTGAAAAGCTG 500

Qy  121 GluProGlnAlaAlaValAlaLysAlaLeuGlyGluAspIleLeuLeuGlnTrpMet 140
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  501 GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAGGACATTCTTCTGCAATGGATG 560

Qy  141 GluGluThrGlu 144
        ||||||||||||
Db  561 GAGGAGACAGAA 572
```

RESULT 6

```
ID   ADG46668 standard; DNA; 926 BP.
XX
AC   ADG46668;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Human Zcyto10 DNA #1.
XX
KW   cytokine-like polypeptide-10; Zcyto10; wound healing;
KW   platelet proliferation; wound repair; mucous production; asthma;
KW   bronchitis; tracheobronchial tract disease; periodontal disease;
KW   skin condition; psoriasis; eczema; dry skin; protein therapy; human;
KW   vulnerary; respiratory; antibronchitic; dental; dermatological; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             45..575
FT                   /*tag= b
FT                   /product= "Human Zcyto10 protein"
FT   sig_peptide     45..116
FT                   /*tag= a
FT   mat_peptide     117..572
FT                   /*tag= c
FT                   /product= "Human mature Zcyto10 protein"
XX
XX
PN   US2003176657-A1.
XX
PD   18-SEP-2003.
XX
PF   15-APR-2003; 2003US-00413661.
XX
PR   26-NOV-1997; 97US-00665997P.
PR   25-NOV-1998; 98US-00199586.
PR   17-MAY-1999; 99US-00313458.
XX
PA   (CONK/) CONKLIN D C.
PA   (HALD/) HALDEMAN B A.
XX
PI   Conklin DC, Haldeman BA;
XX
PF   WPI; 2003-863865/80.
DR   P-PSDB; ADG46669, ADG46679.
XX
PT   Novel isolated mammalian cytokine-like polypeptide-10 (Zcyto10), useful
PT   for treating asthma, bronchitis and other tracheobronchial damage.
XX
PS   Disclosure; SEQ ID NO 1; 31pp; English.
XX
CC   The present invention relates to novel mammalian cytokine-like
CC   polypeptide-10 (Zcyto10) proteins and polynucleotides encoding such
CC   proteins. Sequences of the invention are useful for promoting the healing
CC   of wounds and for stimulating the proliferation of platelets. In
CC   particular Zcyto10 polypeptides may be used in trachea-specific or
CC   tracheobronchial-specific applications such as maintenance or wound
CC   repair of the tracheobronchial epithelium or cells underlying it; in
CC   regulating mucous production; mucociliary clearance of debris; in
CC   treatment of asthma, bronchitis and other diseases of the
CC   tracheobronchial tract. They are also used to promote regeneration of
CC   affected tissues which may be especially useful in the treatment of
CC   periodontal disease. Zcyto10 polypeptides can be used to treat skin
CC   conditions such as psoriasis, eczema and dry skin in general. They are
CC   also used in protein therapy. The present sequence is human Zcyto10 DNA.
XX
SQ   Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;
```

```
Alignment Scores:
Pred. No.:
Score:                    1.17e-86     Length:         926
Percent Similarity:       753.00       Matches:        144
Best Local Similarity:    100.00%      Conservative:   0
Query Match:              100.00%      Mismatches:     0
DB:                       10           Indels:         0
                                       Gaps:           0

US-10-789-129-26 (1-144) x ADG46668 (1-926)

Qy    1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  141 TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCGACATACGGGGCAGT 200

Qy   21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgThrGluSerLeuGln 40
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  201 GTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGACTGAGTCTTTGCAA 260

Qy   41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  261 GACACAAAGCCTGCAAATCGATGCTGCCTCCTGCGCCATTTGCTTAAGACTCTACTGGAC 320

Qy   61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  321 AGGGTATTTAAAAACTACCAGACACCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC 380

Qy   81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisSerAlaHisMetThrCys 100
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  381 GCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTGTCCATGCCCACACATGACATGC 440
```

```
Qy   101  HisCysGlyGluGluAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu  120
          |||||||||||||||||||||||||||||||||||||||||
Db   441  CATTGTGGGGAGGAGGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG  500

Qy   121  GluProGlnAlaAlaValAlaValLysAlaLeuGlyGluLeuGluAspIleLeuLeuGlnMet  140
          |||||||||||||||||||||||||||||||||||||||||
Db   501  GAACCTCAGGCAGCAGTGTGAAGGCTTTGGGGGAACTAGACAATTCTTCGACAATGGATG  560

Qy   141  GluGluThrGlu  144
          |||||||||||
Db   561  GAGGAGGACAGAA  572
```

RESULT 7

```
ID   ADQ88066       standard; DNA; 926 BP.
XX
AC   ADQ88066;
XX
DT   07-OCT-2004  (first entry)
XX
DE   Human Zcyto10 longer form DNA.
XX
KW   Mammalian cytokine-like polypeptide-10; Zcyto10; cell proliferation;
KW   cell differentiation; cytokine production; autoimmune disease;
KW   insulin dependent diabetes mellitus; multiple sclerosis;
KW   rheumatoid arthritis; cancer; wound healing; tissue regeneration;
KW   platelet count; asthma; skin disease; psoriasis; eczema; dry skin;
KW   antidiabetic; neuroprotective; antirheumatic; antiarthritic; cytostatic;
KW   immunostimulant; vulnerary; antiasthmatic; antipsoriatic; dermatological;
KW   gene therapy; human; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             45..575
FT                   /tag= b
FT                   /product= "Human Zcyto10 protein"
FT   sig_peptide     45..116
FT                   /tag= a
FT   mat_peptide     117..572
FT                   /tag= c
FT                   /product= "Human mature Zcyto10 protein"
FT   CDS             141..575
FT                   /tag= d
FT                   /product= "Human Zcyto10 protein fragment"
FT                   /partial
FT                   /note= "No start codon"
XX
PN   US2004142428-A1.
XX
PD   22-JUL-2004.
XX
PF   27-FEB-2004; 2004US-00789129.
XX
PR   26-NOV-1997;    97US-0065997P.
PR   25-NOV-1998;    98US-00199586.
PR   15-APR-2003; 2003US-00413661.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Conklin DC, Haldeman BA;
XX
DR   WPI; 2004-552564/53.
DR   P-PSDB; ADQ88067, ADQ88077, ADQ88091.
XX
PT   New Zcyto10 polypeptides and polynucleotides, useful for treating
PT   autoimmune diseases (e.g. insulin dependent diabetes mellitus, multiple
PT   sclerosis or rheumatoid arthritis), or skin conditions (e.g. psoriasis or
PT   eczema).
XX
PS   Disclosure; SEQ ID NO 1; 31pp; English.
XX
```

```
CC   The present invention provides mammalian cytokine-like polypeptide-10
CC   (Zcyto10) proteins and their encoding polynucleotides. The invention is
CC   useful for treating conditions characterised by improper cell
CC   proliferation, cell differentiation or cytokine production, specifically
CC   for treating autoimmune diseases such as insulin dependent diabetes
CC   mellitus, multiple sclerosis and rheumatoid arthritis and for inhibiting
CC   cancer cell growth. The invention is also used to stimulate the immune
CC   system, to enhance wound healing and promote regeneration of affected
CC   tissues, to increase platelet count and to treat asthma and skin
CC   conditions such as psoriasis, eczema and dry skin. The invention acts as
CC   an antidiabetic, neuroprotective, antirheumatic, antiarthritic,
CC   cytostatic, immunostimulant, vulnerary, antiasthmatic, antipsoriatic and
CC   dermatological agent. The invention is also used in gene therapy. The
CC   present sequence is human Zcyto10 longer form DNA.
XX
SQ   Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;
XX
```

```
Alignment Scores:
Pred. No.:               1.17e-86        Length:         926
Score:                   753.00          Matches:        144
Percent Similarity:      100.00%         Conservative:   0
Best Local Similarity:   100.00%         Mismatches:     0
Query Match:             12              Indels:         0
DB:                                      Gaps:           0
```

```
US-10-789-129-26 (1-144) x ADQ88066 (1-926)

Qy    1  CysValIleAlaThrAsnLeuGlnLeuIleArgAsnGlyPheSerAspIleArgGlySer   20
         ||||||||||||||||||||||||||||||||||||||||
Db  141  TGTGTGATCGCCACAAACCTTCAGCAAAATCAGGAAAATACGAAATGGCGGGGCAGT    200

Qy   21  ValGlnAlaLysAspGlyAsnIleAspPheIleAspGlyIleLeuArgGluAspValAsn   40
         ||||||||||||||||||||||||||||||||||||||||
Db  201  GTGCAAGCCAAAGATGGAAACATTGACATCAGAGAATCTTAAGGAGGAGACTGAGTCTTTGCAA  260

Qy   41  AspThrLysProAlaAsnArgCysSerLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp   60
         ||||||||||||||||||||||||||||||||||||||||
Db  261  GACACAAAAGCCTGCAAACATCGAATGCTGCCTCTGCGCCATTTGCTAAGACTCTATCTGGAC  320

Qy   61  ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu   80
         ||||||||||||||||||||||||||||||||||||||||
Db  321  AGGGTATTTAAAAACTACCAGACACCCTGACCCATTATACTCTCCGGAAGATCAGCAGCCTC  380

Qy   81  AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys   100
         ||||||||||||||||||||||||||||||||||||||||
Db  381  GCCAATTCCTTTCTTACCATCAAGAAAGACCTCCGGCTCTGTCATGCACATGACATGC    440

Qy  101  HisCysGlyGluGluAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu   120
         ||||||||||||||||||||||||||||||||||||||||
Db  441  CATTGTGGGGAGGAGGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG  500

Qy  121  GluProGlnAlaAlaValAlaValLysAlaLeuGlyGluLeuGluAspIleLeuLeuGlnMet  140
         ||||||||||||||||||||||||||||||||||||||||
Db  501  GAACCTCAGGCAGCAGTGTGAAGGCTTTGGGGGAACTAGACAATTCTTCGACAATGGATG  560

Qy  141  GluGluThrGlu  144
         |||||||||||
Db  561  GAGGAGGACAGAA  572
```

RESULT 8

```
ID   ADR16327       standard; DNA; 926 BP.
XX
AC   ADR16327;
XX
DT   21-OCT-2004  (first entry)
XX
DE   Human cytokine-like polypeptide-10.
XX
KW   Cytokine-like polypeptide-10; Zcyto10; therapy; asthma; infection;
KW   psoriasis; eczema; dry skin; wound healing; platelet proliferation;
KW   human; gene; ds.
XX
```

```
OS   Homo sapiens.
XX
FH   Key              Location/Qualifiers
FT   CDS              45..575
                      /*tag= b
FT   sig_peptide      45..116
                      /product= "Zcyto10 long form protein"
                      /*tag= a
FT   mat_peptide      117..572
                      /*tag= c
                      /product= "Mature Zcyto10 long form protein"
XX
PN   US2004152878-A1.
XX
PD   05-AUG-2004.
XX
PF   27-FEB-2004; 2004US-00789968.
XX
PR   26-NOV-1997; 97US-0066597P.
PR   25-NOV-1998; 98US-00199586.
PR   15-APR-2003; 2003US-00413561.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Conklin DC, Haldeman BA;
XX
DR   WPI; 2004-580197/56.
DR   P-PSDB; ADR16328, ADR16338.
XX
PT   New isolated antibody that binds to a Zcyto10 polypeptide, useful for
PT   treating asthma, microbial or viral infections, and for promoting the
PT   healing of wounds, psoriasis, eczema or dry skin.
XX
PS   Disclosure; SEQ ID NO 1; 32pp; English.
CC
CC   The invention relates to novel cytokine-like polypeptide-10 (Zcyto10)
CC   polypeptides and polynucleotides. Zcyto10 sequences are useful for
CC   treating asthma, microbial or viral infections, psoriasis, eczema or dry
CC   skin, for promoting the healing of wounds and for stimulating the
CC   proliferation of platelets. The present sequence is human Zcyto10 DNA.
XX
SQ   Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:
Score:                 1.17e-86          Length:        926
Percent Similarity:    753.00            Matches:       144
Best Local Similarity: 100.00%           Conservative:  0
Query Match:           100.00%           Mismatches:    0
DB:                    13                Indels:        0
                                         Gaps:          0

US-10-789-129-26 (1-144) x ADR16327 (1-926)

Qy    1  CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer  20
Db  141  TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGACATACGGGGGCAGT 200

Qy   21  ValGlnAlaLysAspGlyAsnIleAspIleLeuArgIleLeuArgArgThrGluSerLeuGln 40
Db  201  GTGCAAGCCAAAGATGGAAACATTGACATCTTAAGGAGACTGAGTCTTTGCAA 260

Qy   41  AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
Db  261  GACACAAAGCCTGCAAATCGATGCTGCCTCCTGCGGCATTTGCTAAGACTCTACTGGAC 320

Qy   61  ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
Db  321  AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC 380

Qy   81  AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
Db  381  GCCAATTCCTTCTTTACCATCAAGAAGGAGACCTCGCGCTCTGTCATGCCCACACATGC 440
```

```
Qy  101  HisCysGlyGluGluLeuAlaMetLysLysTyrSerGlnIleIleLeuLeuSerHisPheGluLysLeu 120
Db  441  CATTGTGGGGCGGAGAAGAACATGAAGAGAAATACAGCCAGATTCTGACTCACTTTGAAAAAGCTG 500

Qy  121  GluProGlnAlaAlaValValValLysAlaLeuGluLeuGluTrpMet 140
Db  501  GAACCTCAGGCAGCCAGGTTGTGAAGGCTTTGGGGGGAACTGAGACAATTCTTCTGCAAATGATG 560

Qy  141  GluGluThrGlu 144
Db  561  GAGGAGACAGAA 572


RESULT 9
ADR24325
ID   ADR24325 standard; DNA; 926 BP.
XX
AC   ADR24325;
XX
DT   21-OCT-2004 (first entry)
XX
PN   WO2004065545-A2.
XX
PD   05-AUG-2004.
XX
PF   15-JAN-2004; 2004WO-US001100.
XX
PR   15-JAN-2003; 2003US-00342887.
XX
PA   (ROSE-) ROSETTA INPHARMATICS LLC.
PA   (NECA-) NETHERLANDS CANCER INST.
XX
PI   Van't Veer LJ, He Y;
XX
DR   WPI; 2004-593473/57.
XX
OS   Homo sapiens.
XX
DE   Breast cancer prognosis marker #186.
XX
KW   ds; breast cancer; prognosis; gene expression; diagnosis.
XX
PT   Classifying a breast cancer patient according to prognosis comprises
PT   determining the similarity between the level of expression of each of
PT   five genes in a cell sample taken from patient, to control levels.
XX
PS   Disclosure; SEQ ID NO 186; 226pp; English.
CC
CC   The invention relates to a method of classifying a breast cancer patient
CC   according to prognosis by determining the similarity between the level of
CC   expression of each of five genes for which markers are listed in the
CC   specification, in a cell sample taken from the breast cancer patient, to
CC   control levels of expression for each respective five genes to obtain a
CC   patient similarity value. The methods are useful for classifying a breast
CC   cancer patient according to prognosis. Kits and computer program products
CC   are useful for data analysis using the diagnostic, prognostic and
CC   statistical methods of the invention. This sequence corresponds to a
CC   marker used in the method of the invention.
XX
SQ   Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:
Score:                 1.17e-86          Length:        926
Percent Similarity:    753.00            Matches:       144
Best Local Similarity: 100.00%           Conservative:  0
Query Match:           100.00%           Mismatches:    0
DB:                    13                Indels:        0
                                         Gaps:          0

US-10-789-129-26 (1-144) x ADR24325 (1-926)

Qy    1  CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer  20
Db  141  TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGACATACGGGGGCAGT 200
```

```
Qy    21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgThrGluSerLeuGln 40
         ||||||||||||||||||||||||||||||||||||||||
Db   201 GTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGACTGAGTCTTTGCAA 260

Qy    41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
Db   261 GACACAAAGCCTGCGAATCGATGCTGCCTCCTCCGGCGCCATTTGCTACTTATCTGGAC 320

Qy    61 ArgValPheLysAsnTyrGlnThrProAspHisHisTyrThrLeuArgLysLeuSerSerLeu 80
Db   321 AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC 380

Qy    81 AlaAsnSerPheLeuThrIleLysLysAspAspLeuArgLeuCysHisIleAlaHisMetThrCys 100
Db   381 GCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTGTCATGCCCACATGACATGC 440

Qy   101 HisCysGlyGluGluLysAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu 120
Db   441 CATTGTGGGGGAGGAGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG 500

Qy   121 GluProGlnAlaAlaValAlaValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet 140
Db   501 GAACCTCAGGCAGCCGTGGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATG 560

Qy   141 GluGluThrGlu 144
Db   561 GAGGAGACAGAA 572
```

RESULT 10
ADS18362

```
ID   ADS18362 standard; DNA; 926 BP.
XX
AC   ADS18362;
XX
DT   02-DEC-2004 (first entry)
XX
DE   Human Zcyto10 protein encoding DNA #1.
XX
KW   Zcyto10; cytokine-like polypeptide; cell proliferation;
KW   cell differentiation; autoimmune disease; multiple sclerosis;
KW   rheumatoid arthritis; asthma; psoriasis; diabetes; cancer; wound; gene therapy;
KW   immunosuppressive; antidiabetic; neuroprotective; antirheumatic;
KW   antiarthritic; antiasthmatic; antipsoriatic; cytostatic; vulnerary;
KW   human; gene; chromosome 1q32.2; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FH
FT   CDS             45..575
FT                   /*tag= b
FT                   /product= "Zcyto10 protein "
FT   sig_peptide     45..116
FT                   /*tag= a
FT   mat_peptide     117..572
FT                   /*tag= c
FT                   /product= "Mature Zcyto10 protein"
XX
SQ   Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;
```

```
XX
DR   WPI; 2004-667683/65.
DR   P-PSDB; ADS18363, ADS18373.
XX
PT   New antibody that selectively binds to a mammalian cytokine-like polypeptide,
PT   Zcyto10 polypeptide useful for modulating cell proliferation, cell differentiation or cytokine
PT   production in the prevention or treatment of e.g. autoimmune diseases,
PT   cancer or wounds.
XX
PS   Disclosure; SEQ ID NO 1; 31pp; English.
XX
CC   The present invention relates to a mammalian cytokine-like polypeptide,
CC   Zcyto10 and its encoding polynucleotide. The invention is useful for
CC   modulating cell proliferation, cell differentiation or cytokine
CC   production in the prevention or treatment of conditions such as
CC   autoimmune diseases (e.g. diabetes, multiple sclerosis, rheumatoid
CC   arthritis, asthma or psoriasis) and cancer or wounds. The invention is
CC   also useful in gene therapy. The present sequence is the human Zcyto10
CC   protein encoding DNA. This Zcyto10 gene is located on chromosome 1q32.2.
XX
SQ   Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;
```

US-10-789-129-26 (1-144) x ADS18362 (1-926)

Alignment Scores:

Pred. No.:	1.17e-86	Length:	926
Score:	753.00	Matches:	144
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	13	Indels:	0
DB:		Gaps:	0

```
Qy     1 CysValIleAlaThrAsnLeuGlnGluIleLeuArgAsnGlyPheSerAspIleArgGlySer 20
         ||||||||||||||||||||||||||||||||||||||||
Db   141 TGTGTGGATCGCCACAAACCTTCAGGGAAATACGAAATGGATTTTCTGACATACGGGGCAGT 200

Qy    21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgThrGluSerLeuGln 40
Db   201 GTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGACTGAGTCTTTGCAA 260

Qy    41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
Db   261 GACACAAAGCCTGCGAATCGATGCTGCCTCCTCCGGCGCCATTTGCTACTTATCTGGAC 320

Qy    61 ArgValPheLysAsnTyrGlnThrProAspHisHisTyrThrLeuArgLysLeuSerSerLeu 80
Db   321 AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC 380

Qy    81 AlaAsnSerPheLeuThrIleLysLysAspAspLeuArgLeuCysHisIleAlaHisMetThrCys 100
Db   381 GCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTGTCATGCCCACATGACATGC 440

Qy   101 HisCysGlyGluGluLysAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu 120
Db   441 CATTGTGGGGGAGGAGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG 500

Qy   121 GluProGlnAlaAlaValAlaValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet 140
Db   501 GAACCTCAGGCAGCCGTGGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATG 560

Qy   141 GluGluThrGlu 144
Db   561 GAGGAGACAGAA 572
```

RESULT 11
AEA50048

```
ID   AEA50048 standard; cDNA; 926 BP.
XX
AC   AEA50048;
XX
DT   11-AUG-2005 (first entry)
XX
DE   Full length IL-20 coding sequence.
```

XX
SS; gene; Antiinflammatory; Gastrointestinal-Gen.; Antiulcer;
KW Antiarthritic; Dermatological; Antipsoriatic; Antibacterial;
KW Immunosuppressive; Antimicrobial; IL-Antagonist-20; interleukin-20;
KW IL-20; inflammation; inflammatory bowel disease; ulcerative colitis;
KW Crohns disease; arthritis; atopic dermatitis ; psoriasis; endotoxemia;
KW septicemia; toxic shock syndrome ; infectious disease.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   45. .575
FT   /*tag= a
XX
PN WO2005052000-A2.
XX
PD 09-JUN-2005.
XX
PF 19-NOV-2004; 2004WO-US039071.
XX
PR 21-NOV-2003; 2003US-0524131P.
PR 24-MAR-2004; 2004US-0555857P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Xu W, Kindsvogel WR, Chen Z, Hughes SD, Chandrasekher YA;
PI Dillon SR, Lehner JM, Siadak AW, Sivakumar PV, Moore MD;
XX
DR WPI; 2005-403359/41.
DR P-PSDB; ABA50049, ABA50050.
XX
PT Producing an antibody to an interleukin-20 (IL-20) polypeptide, useful
PT for treating inflammatory diseases e.g., Crohn's disease, by inoculating
PT an animal with the polypeptide eliciting an immune response to produce
PT the antibody.
XX
XX
Example 1: SEQ ID NO 1; 268pp; English.
XX
CC This sequence encodes full length interleukin-20 (IL-
CC 20x1. The method of the invention for producing an antibody to IL-20
CC comprises inoculating an animal with an IL-20 polypeptide which elicits
CC an immune response in the animal to produce the antibody, and isolating
CC the antibody from the animal. The antibody is useful for treating a
CC pathological condition in a subject associated with IL-20 activity such
CC as chronic inflammatory condition, specifically inflammatory bowel
CC disease, ulcerative colitis, Crohns' disease, arthritis, atopic
CC dermatitis and psoriasis, or acute inflammatory condition such as
CC endotoxemia, septicemia, toxic shock syndrome and infectious disease. An
CC antagonist of IL-20 is useful for treating a mammal afflicted with an
CC inflammatory disease in which IL-20 plays a role such that the
CC inflammation is reduced, where the antagonist comprises an antibody,
CC antibody fragment, or binding polypeptide that specifically binds a
CC polypeptide or polypeptide fragment of IL-20 or a polypeptide
CC polypeptide fragment of IL-20, and where the inflammatory activity of IL-
CC 20 is reduced. The method is useful for producing such therapeutic
CC antibody. The antibody or antibody fragment, produced using the above
CC method, binds to IL-20, and inhibits or reduces the pro-inflammatory
CC activity of IL-20. IL-20-induced proliferation or differentiation of
CC hematopoietic cells and hematopoietic cell progenitors may be reduced or
CC inhibited using the antibody.
XX
SQ Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:
Score: 1.17e-86
Score: 753.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 14

Length: 926
Matches: 144
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-10-789-129-26 (1-144) x ABA50048 (1-926)

Qy   1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 141 TGTGTGGATCGCCACAAACCTTCAGGAAATACCAGAAATGGATTTTCTGACATACGGGAGT 200

Qy 21 ValGlnHisAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 201 GTGCAGCACGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAA 260

Qy 41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 261 GACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTTAGACTCTATCTGGAC 320

Qy 61 ArgValPheLysAsnTyrGlnThrProAspHisIleTyrThrLeuArgLysIleSerSerLeu 80
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 321 AGGGTATTTAAAAACTACCAGACACCCCGCCATTATACTCTCCGGAAGATCAGCAGCCTC 380

Qy 81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 381 GCCAATTCCTTTCTTACCATCAAGAAGGACCTTCGCCTGTGTCATGCCCACATGACATGC 440

Qy 101 HisCysGlyGlyUlaMetLysSerTyrSerGlnIleLeuSerHisPheGluLysLeu 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 441 CATTGTGGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG 500

Qy 121 GluProGlnAlaIleAalValValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet 140
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 501 GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATG 560

Qy 141 GluGluThrGlu 144
        ||||||||||||
Db 561 GAGGAGACAGAA 572

RESULT 12

ID ABA28786 standard; cDNA; 926 BP.
XX
AC ABA28786;
XX
DT 11-AUG-2005 (first entry)
XX
DE Human interleukin 20 (IL-20) precursor cDNA clone.
XX
KW antibody production; cytokine; antiinflammatory; gastrointestinal-gen.;
KW antiulcer; antiarthritic; dermatological; antipsoriatic; antibacterial;
KW immunosuppressive; antimicrobial; inflammation;
KW inflammatory bowel disease; ulcerative colitis; Crohns disease;
KW arthritis; atopic dermatitis; psoriasis; cancer; endotoxemia; sepsis;
KW endotoxic shock; infectious disease; IL-20; interleukin-20; ss; gene.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   45. .575
FT   /*tag= a
FT   /product= "Human interleukin 20 (IL-20) protein"
XX
PN WO2005052001-A2.
XX
PD 09-JUN-2005.
XX
PF 19-NOV-2004; 2004WO-US039097.
XX
PR 21-NOV-2003; 2003US-0524131P.
PR 24-MAR-2004; 2004US-0555857P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Xu W, Kindsvogel WR, Chen Z, Hughes SD, Chandrasekher YA;
PI Dillon SR, Lehner JM, Siadak AW, Sivakumar PV, Moore MD;
XX
DR WPI; 2005-403360/41.
DR P-PSDB; ABA28787.
XX

```
RESULT 13
ABV75151
ID   ABV75151 standard; DNA; 462 BP.
```

```
PT  Producing an antibody to an interleukin 20RA (IL-20RA) polypeptide,
PT  useful for treating inflammatory diseases e.g., arthritis, by inoculating
PT  an animal with the polypeptide which elicits an immune response to
PT  produce the antibody.
XX
PS  Example 1; SEQ ID NO 1; 265pp; English.
XX
CC  The invention relates to a novel method for producing an antibody to a
CC  polypeptide. The method comprises inoculating an animal with a
CC  polypeptide selected from any of SEQ ID NO: 14, 15, 17 or 19 as given in
CC  the specification, where the polypeptide elicits an immune response in
CC  the animal to produce the antibody, and isolating the antibody from the
CC  animal. The antibody specifically binds to the pro-inflammatory cytokine
CC  interleukin 20 (IL-20 or Zcyto10), or one its receptors IL-20RA (ZcytpR7)
CC  or IL-20RB (pDIRS1). The method of the invention demonstrates
CC  antiinflammatory, gastrointestinal-gen., antiulcer, antiarthritic,
CC  antiinflammatory, anipsoriatic, antibacterial, immunosuppressive and
CC  dermatological, antipsoriatic, antibacterial, immunosuppressive and
CC  antimicrobial applications. The antibody may be useful for treating a
CC  pathological condition in a subject associated with IL-20RA, such as a
CC  chronic inflammatory condition selected from inflammatory bowel disease,
CC  ulcerative colitis, Crohn's disease, arthritis, atopic dermatitis and
CC  psoriasis, cancer, or an acute inflammatory condition such as
CC  endotoxemia, septicemia, toxic shock syndrome and infectious disease. The
CC  current sequence is that of a human IL-20 precursor cDNA clone of the
CC  invention.
XX
SQ  Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;
```

US-10-789-129-26 (1-144) x AEA28786 (1-926)

Alignment Scores:

```
Score:                   1.17e-86
Pred. No.:               753.00
Percent Similarity:      100.00%
Best Local Similarity:   100.00%
Query Match:             14
```

```
                Length:        926
                Matches:       144
                Conservative:  0
                Mismatches:    0
                Indels:        0
                Gaps:          0
```

```
Qy     1 CysValIleAlaThrAsnLeuGlnGlnIleLeuArgAsnGlyPheSerAspIleArgGlySer 20
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   141 TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGACATACGGGCAGT 200

Qy    21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   201 GTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAA 260

Qy    41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuArgLeuTyrLeuAsp 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   261 GACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGGCCATTTGCTAAGACTCTATCTGGAC 320

Qy    61 ArgValPheLysAsnTyrGlnThrProAspHisSerTyrThrLeuArgLysIleSerSerLeu 80
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   321 AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC 380

Qy    81 AlaAsnSerPheLeuThrIleLysLysAspLeuCysHisAlaHisMetThrCys 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   381 GCCAATTCCTTTCTTACCATCAAGAAGGACCTGTGCCACGCCCATGACATGC 440

Qy   101 HisCysGlyGluGluGlnAlaMetLeuLysLeuTyrSerGlnIleLeuSerHisPheGlyLeuSerLeu 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   441 CATTGTGGGGAGGAGCAAGCAAATGAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG 500

Qy   121 GluProGlnAlaAlaValValLysAlaLeuGlyGluGluAspGlyLeuLeuLeuLeuGlnTrpMet 140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   501 GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGAGACAATTCTTCTGCAATGGATG 560

Qy   141 GluGluThrGlu 144
         ||||||||||||
Db   561 GAGGAGACAGAA 572
```

```
XX
AC  ABV75151;
XX
DT  19-FEB-2003  (first entry)
XX
DE  Human interleukin-20 (IL-20) codon optimised fragment zcyto10X1.
XX
KW  Protein synthesis; data mining; recombinant; interleukin-20; IL-20;
KW  human; ds.
XX
OS  Homo sapiens.
XX
PN  WO200028653-A2.
XX
PD  24-OCT-2002.
XX
PF  12-APR-2002; 2002WO-US011513.
XX
PR  13-APR-2001; 2001US-0283688P.
XX
PA  (ZYMO ) ZYMOGENETICS INC.
XX
PI  Powndew TA, Chan C;
XX
DR  WPI; 2003-067576/06.
XX
PT  New polynucleotide, useful for producing a nucleic acid construct for
PT  expression of an amino acid sequence of interest.
XX
PS  Example 1; Page 36; 40pp; English.
XX
CC  The invention provides a new purified polynucleotide that comprises the
CC  nucleic acid sequence A-B-C-D-E; where: A= start codon, B= polynucleotide
CC  sequence of 13 nucleic acids, where the sequence has homology with 13
CC  base pair (bp) sequence, where at least 5 nucleic acids are identical to
CC  a 13 bp sequence (ABV75139), and where the nucleic acid sequence does not
CC  code for a stop codon, C= polynucleotide sequence comprising 10, 13, 16
CC  or 19 nucleic acids of a 19 bp sequence (ABV75140), D= polynucleotide
CC  sequence comprising 8 bp (ABV75141), E= polynucleotide sequence selected
CC  from 9 sequences (ABV75144-150) where at least 50% nucleotides are either
CC  adenine or thymine, and where only E encodes a stop codon. The
CC  polynucleotide is useful for producing a nucleic acid construct for
CC  expression of an amino acid sequence of interest. The present sequence
CC  represents a human interleukin-20 (IL-20) codon optimised fragment for
CC  expression in E. coli
XX
SQ  Sequence 462 BP; 121 A; 131 C; 93 T; 0 U; 0 Other;
```

US-10-789-129-26 (1-144) x ABV75151 (1-462)

Alignment Scores:

```
Score:                   1.38e-86
Pred. No.:               749.00
Percent Similarity:      100.00%
Best Local Similarity:   99.47%
Query Match:             8
```

```
                Length:        462
                Matches:       143
                Conservative:  0
                Mismatches:    1
                Indels:        0
                Gaps:          0
```

```
Qy     1 CysValIleAlaThrAsnLeuGlnGlnIleLeuArgAsnGlyPheSerAspIleArgGlySer 20
         ||||||||||||||||||||||||||||||||||||||||| ::||||||||||||||||||||
Db    28 TGTGTGATCGCCACCAACCTGCAGCAGAAATCCGTAAGGGGTTTCTGAGATCCGTGGCAGC 87

Qy    21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    88 GTGCAGGCCAAAGATGGTAACATTGACATCCGTATCCTGCGTCGTACCGAGTCTCTGCAG 147

Qy    41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuArgLeuTyrLeuAsp 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   148 GACACCAAACCGGCGAACCGTTGCTGCCTGCTGCGCCACCTGCGTCTGTATCTGGAC 207

Qy    61 ArgValPheLysAsnTyrGlnThrProAspHisSerTyrThrLeuArgLysIleSerSerLeu 80
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   208 CGTGTGTTTCAAAAACTACCAGACCCCGGACCACTATACCCTGCGTAAAATCAGCAGCCTG 267
```

Score:
Pred. No.:
Alignment Scores:

```
SQ   Sequence 462 BP; 121 A; 131 C; 117 G; 93 T; 0 U; 0 Other;
        strength.
CC   (IL)-20 DNA. This sequence is used in the comparison of promoter
CC   expression of target genes. The present sequence is the human interleukin
CC   Escherichia coli expression system. They are useful for controlling basal
CC   toxic and interfere with production of recombinant protein from an
CC   useful for controlling uninduced, leaky expression of proteins that are
CC   proteins. The Syn 1 and Syn 2 tight regulated synthetic promoters are
CC   promoters and methods for enhancing the expression of recombinant
CC   The invention relates to Syn 1 and Syn 2 tight regulated synthetic
XX
PS   Example 5; SEQ ID NO 18; 39pp; English.
XX
PT   expression system.
PT   interfere with production of recombinant protein from an Escherichia coli
PT   controlling uninduced, leaky expression of proteins that are toxic and
PT   New Syn 1 and Syn 2 tight regulated synthetic promoters, useful for
XX
PN   WO2005058946-A2.
XX
PD   30-JUN-2005.
XX
PR   12-DEC-2003; 2003US-0529412P.
XX
PF   10-DEC-2004; 2004WO-US041776.
XX
PI   Chan C,   Powder TA;
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
DT   08-SEP-2005 (first entry)
XX
AC   AEB26649;
XX
ID   AEB26649 standard; DNA; 462 BP.
XX
RESULT 14
AEB26649
```

```
Db   448 GAGGAGGACCGAA 459
        ||||||||||||
Qy   448 GAGGAGGACCGAA 459

Db   388 GAACCGGCAGGCAGCGAGTGGTGAAAAGCTTCTGGGGTGAACTGGACAATTCTGCTGGTGGATG 447
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   141 GluGluThrGlu 144

Db   328 CACTGTGGTGAGGAGGCAATGAAAAAATACAGCCAGATTCTGAGCCACTTCAAAAACTG 387
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   121 GluProGlnAlaAlaValValLeuLysAlaAlaLeuGlyGluLeuAspIleIleLeuLeuGlnInTrpMet 140

Db   268 GCCAACTCCTTCCTGACCATCAAAAAAGACCTGAGCGGTCGTCAGTCAGCCCACATGACCTGC 327
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   101 HisCysGlyGluGluLysHisAlaMetLysTyrSerGlnIleLeuSerHisPheGlyLysLeu 120

Db   388 GAACCGGCAGGCAGCGAGTGGTG...
Qy   81  AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
```

(partial sequence alignment data)

```
KW   Expression; gene regulation; toxin; interleukin; gene; ds.
XX
OS   Homo sapiens.
OS
FH   Key
FT   CDS             1..462
FT                   /tag= a
FT                   /product= "Human interleukin (IL)-20"
XX
DE   Human interleukin (IL)-20 DNA, SEQ ID NO: 18.
XX
```

```
Percent Similarity:   100.00%   Conservative:   1
Best Local Similarity:   99.31%   Mismatches:   0
Query Match:   99.47%   Indels:   0
DB:   14   Gaps:   0

US-10-789-129-26 (1-144) x AEB26649 (1-462)
```

```
Qy   1   CysValIleIleAlaThrAsnLeuLeuGlnGluIleIleLeuArgAsnGlyPheSerAspArgGlySer 20
        |||||||||||||||||||||||||||||||||||||||||||||::::|||||||||||||||
Db   208 CGTGTTTTTCAAAAACTACCAGACCCCCGGCACACTATACCTTGCGGTAAAATCCGGCTG 267

Qy   61  ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysLysIleSerSerLeu 80
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   148 GACACCAAACCGGCAAACCGGTTGCTCGCCTCGCCGCCACCTTCGCGTCTGTTATCTGGAC 207

Qy   41  AspThrLysProAlaAsnArgCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   88  GTGCAGGCCAAAGATGGTAACATTGACATCCGTATCCTGGGTGTTCTTCGTCTGTACCGAGTTCTCTGGAG 147

Qy   21  ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgAlaThrGluSerLeuGln 40
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   28  TGTGTGATCGGCCACCAACCTGCAGGAAAATCCGTAACGGTTCTCTGAGATCCGGCAGC 87

Qy   81  AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   268 GCCAACTCCTTCCTGACCATCAAAAAAGACCTGAGCGGTCGTCAGTCAGCCCACATGACCTGC 327

Qy   101 HisCysGlyGluGluLysHisAlaMetLysTyrSerGlnIleLeuSerHisPheGlyLysLeu 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   328 CACTGTGGTGAGGAGGCAATGAAAAAATACAGCCAGATTCTGAGCCACTTCAAAAACTG 387

Qy   121 GluProGlnAlaAlaValValLeuLysAlaAlaLeuGlyGluLeuAspIleIleLeuLeuGlnInTrpMet 140
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   388 GAACCGGCAGGCAGCGAGTGGTGAAAAGCTTCTGGGGTGAACTGGACAATTCTGCTGGTGGATG 447

Qy   141 GluGluThrGlu 144
        ||||||||||||
Db   448 GAGGAGGACCGAA 459
```

```
Qy   1   CysValIleIle...
        (first entry)
XX
PN   WO20028853-A2.
XX
PD   24-OCT-2002.
XX
PT   12-APR-2002; 2002WO-US011513.
XX
PF   13-APR-2001; 2001US-0283688P.
XX
PI   Powder TA,   Chan C;
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
KW   human; ds.
KW   Protein synthesis; data mining; recombinant; interleukin-20; IL-20;
XX
DE   EC sequence upstream of IL-20 codon optimised fragment zcyto10X1.
XX
DT   19-FEB-2003 (first entry)
XX
AC   ABV75154;
XX
ID   ABV75154 standard; DNA; 513 BP.
ABV75154
RESULT 15
```

```
OS   Homo sapiens.
OS
XX
PS   Example 1; Page 37; 40pp; English.
XX
PT   expression of an amino acid sequence of interest.
PT   New polynucleotide, useful for producing a nucleic acid construct for
XX
DR   WPI; 2003-067576/06.
```

Score: 749.00   Length: 462   Matches: 143
Pred. No.:   1.38e-86

```
XX
CC   The invention provides a new purified polynucleotide that comprises the
CC   nucleic acid sequence A-B-C-D-E; where: A= start codon, B= polynucleotide
CC   sequence of 13 nucleic acids, where the sequence has homology with 13
CC   base pair (bp) sequence, where at least 5 nucleic acids are identical to
CC   a 13 bp sequence (ABV75139), and where the nucleic acid sequence does not
CC   code for a stop codon, C= polynucleotide sequence comprising 10, 13, 16
CC   or 19 nucleic acids of a 19 bp sequence (ABV75140), D= polynucleotide
CC   sequence comprising 8 bp (ABV75141), E= polynucleotide sequence selected
CC   from 9 sequences (ABV75144-150) where at least 50% nucleotides are either
CC   adenine or thymine, and where only E encodes a stop codon. The
CC   polynucleotide is useful for producing a nucleic acid construct for
CC   expression of an amino acid sequence of interest. The present sequence
CC   represents a sequence comprising an expression cassette (EC)
CC   polynucleotide sequence inserted upstream of a human interleukin-20 (IL-
CC   20) codon optimised sequence fragment for expression in E. coli
XX
SQ   Sequence 513 BP; 143 A; 145 C; 126 G; 99 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:          1.61e-86
Score:              749.00
Percent Similarity: 100.00%          Length:        513
Best Local Similarity: 99.31%        Matches:       143
Query Match:        99.47%           Conservative:  1
                                     Mismatches:    0
DB:                                  Indels:        0
                                     Gaps:          0

US-10-789-129-26 (1-144) x ABV75154 (1-513)

Qy     1 CysValIleAlaThrAsnLeuGlnGlnIleArgAsnGlyPheSerAspIleArgGlySer   20
         ||||||||||||||||||||||||||||||||||||||::::|||||||||||||||||||
Db    79 TGTGTGATCGCCACCAACCTGCAGGAAATCCGTAACGGTTTCTCTGAGATCCGTGGCAGC  138

Qy    21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln   40
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   139 GTGCAGGCCAAAGATGGTAACATTGACATCCGTATCCTGCGTCGTACCGAGTCTCTGCAG  198

Qy    41 AspThrLysProAlaAlaAsnArgCysCysLeuLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   199 GACACCAAAACCGGCAAACCGTTGCTGCTGCTGCTGCGTCACCTGCTGCGTCTGTATCTGGAC  258

Qy    61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu   80
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   259 CGTGTTTTCAAAAACTACCAGACCCCGGACCACTATACCCTGCGTAAAATCAGCAGCCTG  318

Qy    81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys  100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   319 GCCAACTCCTTCCTGACCATCAAAAAAGACCTGCGTCTGTGTCACGCCCACATGACCTGC  378

Qy   101 HisCysGlyGlyGluGlnAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu  120
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   379 CACTGTGGTGAGGAAGCAAATGAAAAAATACAGCCAGATTCTGAGCCACTTCGAAAAACTG  438

Qy   121 GluProGlnAlaAlaValValLysLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet  140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   439 GAACCGCAGGCAGCAGTGGTGAAAGCTTCGGGTGAACTGGACATTCTGCTGCAGTGGATG  498

Qy   141 GluGluThrGlu  144
         ||||||||||||
Db   499 GAGGAGACCGAA  510

Search completed: December 28, 2005, 14:19:32
Job time : 503 secs
```

OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.6
Copyright (c) 1993 - 2005, Compugen Ltd.

Run on: December 28, 2005, 13:52:03 ; Search time 3790 Seconds
(without alignments)
1777.662 Million cell updates/sec

```
Title:          US-10-789-129-26
Perfect score:  753
Sequence:       1 CVIATNLQEIRNGFSDIRGS.........AVVKALGELDILLQWMEETE 144

Scoring table:  BLOSUM62
                Xgapop  10.0 , Xgapext  0.5
                Ygapop  10.0 , Ygapext  0.5
                Fgapop   6.0 , Fgapext  7.0
                Delop    6.0 , Delext   7.0

Searched:       41078325 seqs, 2339541228 residues
Total number of hits satisfying chosen parameters:    82156650

Minimum DB seq length: 0
Maximum DB seq length: 200000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters: -DEV=xlp
-MODEL=frame+_p2n.model
-Q=/ccgn2_1/USPTO_spool_p/US10789129//runat_23122005_152720_20276/app_query.fasta_1.327
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000000
-USER=US10789129 @CGN 1 1 8010 @runat 23122005 152720 20276 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :  EST:*
     1:  gb_est1:*
     2:  gb_est2:*
     3:  gb_est3:*
     4:  gb_htc:*
     5:  gb_est4:*
     6:  gb_est5:*
     7:  gb_est6:*
     8:  gb_est7:*
     9:  gb_gss1:*
    10:  gb_gss2:*
    11:  gb_gss3:*
```

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	749	99.5	531	10	AY402693	AY402693 Homo sapi
2	603	80.1	531	10	AY402694	AY402694 Pan trogl
3	565	75.0	531	10	AY402695	AY402695 Mus muscu
4	547	72.6	1189	4	AK078698	AK078698 Mus muscu
5	461	61.2	676	2	BB624019	BB624019 Mus muscu
6	328	43.6	647	2	CR985515	CR985515 Homo sapi
7	328	43.6	695	1	BB064801	BB064801 Homo sapi
8	328	43.6	699	7	CR992594	CR992594
9	275	36.5	762	6	CA309757	UI-H-FT1-
10 (c)	273	36.3	564	2	BF738279	PM4-KT004
11	265	35.2	748	6	CA306626	UI-H-FT1-
12	229	30.4	709	2	BB639581	BB639581
13	228.5	30.3	897	7	CK800046	AGENCOURT
14	217	28.8	658	6	CD366952	UI-H-FT2-
15	206.5	27.4	538	1	AW635131	b129g02.w
16	206.5	27.4	703	1	AW637118	b154f02.w
17	202.5	26.9	621	11	DQ047027	Homo sapi
18 (c)	202.5	26.9	626	6	CR601530	full-leng
19	198.5	26.4	915	1	AL545939	full-leng
20	197.5	26.2	626	6	CD623370	56738853H
21	196.5	26.1	622	1	AW949784	EST361854
22	190.5	25.3	763	2	BG189587	RST8632 A
23	189.5	25.2	593	1	AW949792	EST361862
24 (c)	187.5	24.9	500	6	CB712018	AMGNNUC:S
25	173	23.0	292	5	BX096099	BX096099
26	166.5	22.1	1024	1	AL571517	AL571517
27	151	20.1	537	10	AY410235	Homo sapi
28 (c)	149	19.8	537	10	AY410236	Pan trogl
29	145.5	19.3	727	8	CX789095	Sa_mx0_74
30	144	19.1	537	10	AY410237	Mus muscu
31	144	19.1	590	1	AA607494	vm61h05.r
32	136	18.1	585	6	CB442949	693798 MA
33	136	18.1	619	7	CO259318	4130740 B
34	134	17.8	337	1	CO259918	EST50599
35	132	17.5	534	10	AY410226	Homo sapi
36	132	17.5	666	9	BG538741	602566998
37	130.5	17.3	487	9	AZ224186	RPCI-23-9
38	130	17.3	709	9	BH299670	CH230-104
39	129	17.1	1655	9	BC022315	Homo sapi
40	127.5	16.9	478	7	CV025407	3079 Full
41	127	16.9	534	10	AY410227	Pan trogl
42 (c)	125.5	16.7	629	7	CF896842	A0216CD02-
43	118.5	15.7	778	6	CF127430	UI-HF-ET0
44	118	15.7	317	1	AJ666110	UI-H-FT1-
45	118	15.7	352	1	AJ668492	AJ668492

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
AY402693
AY402693

```
LOCUS       AY402693                531 bp    DNA     linear   GSS 15-DEC-2003
DEFINITION  Homo sapiens IL20 gene, VIRTUAL TRANSCRIPT, partial sequence.
ACCESSION   AY402693
VERSION     AY402693.1  GI:39758676
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 531)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
  PUBMED    14671302
REFERENCE   2  (bases 1 to 531)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Guide Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
```

them based on alignment.

```
FEATURES            Location/Qualifiers
     source          1..531
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     gene            <1..>531
                     /gene="IL20"
                     /locus_tag="HCM1309"
ORIGIN
```

Alignment Scores:
Pred. No.:

Score:	1.84e-82	Length: 531
	749.00	Matches: 143
Percent Similarity:	100.00%	Conservative: 1
Best Local Similarity:	99.31%	Mismatches: 0
Query Match:	99.47%	Indels: 0
DB:	10	Gaps: 0

US-10-789-129-26 (1-144) x AY402693 (1-531)

```
Qy    1 CysValIleAlaThrAsnLeuGlnGlyIleArgAsnGlyPheSerAspIleArgGlySer 20
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   97 TGTGTGGATCGCCACAAAACCTTCAGGAAATACGAAATGGGATTTCTGAGATACGGGGCAGT 156

Qy   21 ValGlnAlaLysAspGlyAsnIleAspIleLeuArgIleLeuArgThrGluSerLeuGln 40
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  157 GTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAA 216

Qy   41 AspThrLysProAlaAlaAsnArgCysSerLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  217 GACACAAAAGCCTGCGAAATCGATGCTGCCCTCCTGCGGCCATTTGCTAAGACTTCTACTGGAC 276

Qy   41 AspThrLysProAlaAlaAsnArgCysSerLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  277 AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC 336

Qy   61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgGlySerLeuSerLeu 80
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  277 AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC 336

Qy   81 AlaAsnSerPheLeuThrIleLeuTyrGlyLysIleSerAspLeuArgLeuCysHisIleAlaHisMetThrCys 100
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  337 GCCAATTCCTTTCTTACCATCAAGAAGAGGACCTCCGGCTCTTCGTCATGCCCACATGACATGC 396

Qy  101 HisCysSerGlyGluGluIleAlaMetLysGlyLysTyrSerGlnIleIleLeuSerHisPheGluGlyLysLeu 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  397 CATTGTGGGGAGGAAGCAATGAAGAAAATACAGCCAGATTCTGAGTCACTTTGAAAAAGCTG 456

Qy  121 GluProGlnAlaAlaValValLysSerAlaLeuGlyValGluLeuAspIleLeuGlnTrpMet 140
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  457 GAACCTCAGGCAGCAGTTGTGAAGGGCTTTGGGGGAACTAGACATTCTTCGCAATGGATG 516

Qy  141 GluGluThrGlu 144
        |||||||||||
Db  517 GAGGAGACAGA 528
```

RESULT 2
LOCUS   AY402694   531 bp   DNA   linear   GSS 15-DEC-2003
DEFINITION Pan troglodytes IL20 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY402694
VERSION   AY402694.1 GI:39758677
KEYWORDS   GSS.
SOURCE   Pan troglodytes (chimpanzee)
ORGANISM   Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1 (bases 1 to 531)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
TITLE   Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios

JOURNAL   Science 302 (5652), 1960-1963 (2003)
PUBMED   14671302
REFERENCE   2 (bases 1 to 531)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
TITLE   Direct Submission
JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT   This sequence was made by sequencing genomic exons and ordering
            them based on alignment.

```
FEATURES            Location/Qualifiers
     source          1..531
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
     gene            <1..>531
                     /gene="IL20"
                     /locus_tag="HCM1309"
ORIGIN
```

US-10-789-129-26 (1-144) x AY402694 (1-531)

Alignment Scores:
Pred. No.:

Score:	2.65e-64	Length: 531
	603.00	Matches: 118
Percent Similarity:	82.64%	Conservative: 0
Best Local Similarity:	81.94%	Mismatches: 25
Query Match:	80.08%	Indels: 0
DB:	10	Gaps: 0

```
Qy    1 CysValIleAlaThrAsnLeuGlnGlyIleArgAsnGlyPheSerAspIleArgGlySer 20
        ||||||||||||||||||||||||||||||||||||||||||||||||| : ::|||
Db   97 TGTGTGGATCGCCACAAAACCTTCAGGAAATACGAAATGGGATTTCTGAGATACGGGGCAGT 156

Qy   21 ValGlnAlaLysAspGlyAsnIleAspIleLeuArgIleLeuArgThrGluSerLeuGln 40
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  157 GTGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 216

Qy   41 AspThrLysProAlaAlaAsnArgCysSerLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  217 NNNNNNNNNNNNNNNNNNNNNNATCGATGCTGCCCTCCTGCGGCCATTTGCTAAGACTTCTACTGGAC 276

Qy   61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgGlySerLeuSerLeu 80
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  277 AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC 336

Qy   81 AlaAsnSerPheLeuThrIleLeuTyrGlyLysIleSerAspLeuArgLeuCysHisIleAlaHisMetThrCys 100
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  337 GCCAATTCCTTTCTTACCATCAAGAAGAGGACCTCCGGCTCTTCGTCATGCCCACATGACATGC 396

Qy  101 HisCysSerGlyGluGluIleAlaMetLysGlyLysTyrSerGlnIleIleLeuSerHisPheGluGlyLysLeu 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  397 CATTGTGGGGAGGAAGCAATGAAGAAAATACAGCCAGATTCTGAGTCACTTTGAAAAAGCTG 456

Qy  121 GluProGlnAlaAlaValValLysSerAlaLeuGlyValGluLeuAspIleLeuGlnTrpMet 140
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  457 GAACCTCAGGCAGCAGTTGTGAAGGGCTTTGGGGGAACTAGACATTCTTCGCAATGGATG 516

Qy  141 GluGluThrGlu 144
        |||||||||||
Db  517 GAGGAGACAGA 528
```

RESULT 3
LOCUS   AY402695   531 bp   DNA   linear   GSS 15-DEC-2003
DEFINITION Mus musculus IL20 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY402695
VERSION   AY402695.1 GI:39758678
KEYWORDS   GSS.
SOURCE   Mus musculus (house mouse)

ORGANISM   Mus musculus
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
         Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 531)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
         Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
         Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
         Adams,M.D. and Cargill,M.
TITLE   Inferring nonneutral evolution from human-chimp-mouse orthologous
         gene trios
JOURNAL   Science 302 (5652), 1960-1963 (2003)
PUBMED   14671302
REFERENCE   2 (bases 1 to 531)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
         Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
         Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
         Adams,M.D. and Cargill,M.
TITLE   Direct Submission
JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
         Rockville, MD 20850, USA
COMMENT   This sequence was made by sequencing genomic exons and ordering
         them based on alignment.
FEATURES   Location/Qualifiers
     source   1..531
                   /organism="Mus musculus"
                   /mol_type="genomic DNA"
                   /db_xref="taxon:10090"
     gene   <1..>531
                   /gene="IL20"
                   /locus_tag="HCM1309"
ORIGIN

US-10-789-129-26 (1-144) x AY402695 (1-531)

Alignment Scores:
Pred. No.:   1.41e-59
Score: 565.00
Percent Similarity: 85.92%
Best Local Similarity: 76.76%
Query Match: 75.03%
DB: 10

Length: 531
Matches: 109
Conservative: 13
Mismatches: 20
Indels: 0
Gaps: 0

```
Qy      1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
            ||| ||| ::: |||      :::  |||       |||  :::       |||
Db      1 TGTGTGATTACTCCAAACCTACAGCAATACAAAGAGAATTTTCTGAGATTCGGGATAGT 156

Qy     21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
            ||| |||::::||| |     ||||||   |||  |||::||||| ||||||::: :::
Db     97 GTCCAAGCTGAAGATGGAAATATTGACATCAGAGATTTTAAGGACGACTGAGTCTTTGAAA 216

Qy     41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
            ||| |||          ||| |||  |||::  |||  ||| |||   ||||||
Db    217 GACATAAAAGTCTTTGGATAAGGTGCTCGCTTCCTTCGTCATCTAGTGAGAATTCTATCTGAC 276

Qy     61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
            ||| ||| |||       |||::: |||  |||  |||  ||::|||
Db    277 AGGGTATTCAAAGTCTACCAGACCCCTGACCACCATACCCTGAGAAGATCAGCAGCCTC 336

Qy     81 AlaAsnSerPheLeuThrIleLeuLysArgLeuCysHisAlaHisMetThrCys 100
            |||||| ||| ||| |||||| |||||| |||  ||| |||       |||
Db    337 GCCAACTCCTTTCTTATCATCAAGAAGGACCCTCAGTCAGTCATTCACATGGCATGT 396

Qy    101 HisCysGlyGluGlnLeuAlaMetLysLeuTyrSerGlnIleLeuSerHisSpheGluLys 120
            ||| ::||||||||| |||   |||   |||   |||  |||
Db    397 CATTGTGGGGAGCAGAAGCAATGAGAAATTACAACCAAATTCTGAGTCACTTCATAGAGTTG 456

Qy    121 GluProGlnAlaAlaValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet 140
            |||     ||| ||     ||     |||  |||  |||::  :::|||
Db    457 GAACTTCAGGCAGCGGCGGGTGTAAAGGCTTTGGGAGAACTAGGACTTCTTCTGAGATGGATG 516

Qy    141 GluGlu 142
            ||||||
Db    141 GAGGAG 142
```

Db   517 GAGGAG 522

RESULT 4
Db
LOCUS   AK078698   1189 bp   mRNA   linear   HTC 03-APR-2004
DEFINITION   Mus musculus adult male eyeball cDNA, RIKEN full-length enriched
         library, clone:7530415H19 product:interleukin 20, full insert
         sequence.
ACCESSION   AK078698
VERSION   AK078698.1   GI:26098048
KEYWORDS   HTC; CAP trapper.
SOURCE   Mus musculus (house mouse)
ORGANISM   Mus musculus
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
         Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1
AUTHORS   Carninci,P. and Hayashizaki,Y.
TITLE   High-efficiency full-length cDNA cloning
JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
PUBMED   10349636
REFERENCE   2
AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
         Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE   Normalization and subtraction of cap-trapper-selected cDNAs to
         prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
PUBMED   11042159
REFERENCE   3
AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
         Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
         Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
         Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
         Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
         Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
         Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE   RIKEN integrated sequence analysis (RISA) system-384-format
         sequencing pipeline with 384 multicapillary sequencer
JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
PUBMED   11076861
REFERENCE   4
AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
         FANTOM Consortium.
TITLE   Functional annotation of a full-length mouse cDNA collection
JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
         Group Phase I & II Team.
TITLE   Analysis of the mouse transcriptome based on functional annotation
         of 60,770 full-length cDNAs
JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6 (bases 1 to 1189)
AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
         Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
         Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
         Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
         Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
         Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
         Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
         Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
         Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
         Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
         Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
         Muramatsu,M. and Hayashizaki,Y.
TITLE   Direct Submission
JOURNAL   Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
         Physical and Chemical Research (RIKEN), Laboratory for Genome
         Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
         RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
         Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp/,
         URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
         Fax:81-45-503-9216)
COMMENT   cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.

```
FEATURES          Location/Qualifiers
source            1..1189
                  /organism="Mus musculus"
                  /mol_type="mRNA"
                  /strain="C57BL/6J"
                  /db_xref="FANTOM_DB:7530415H19"
                  /db_xref="taxon:10090"
                  /clone="7530415H19"
                  /sex="male"
                  /tissue_type="eyeball"
                  /clone_lib="RIKEN full-length enriched mouse cDNA library"
                  /dev_stage="adult"
misc_feature      227..758
                  /note="interleukin 20 (MGD|MGI:1890473, GB|NM_021380,
                  evidence: BLASTN, 99%, match=826)
                  putative"
polyA_signal      1167..1172
                  /note="putative"
polyA_site        1189
                  /note="putative"
ORIGIN
```

US-10-789-129-26 (1-144) x AK078698 (1-1189)

```
Alignment Scores:
Pred. No.:
Score:                 547.00
Percent Similarity:    84.62%          Length:        1189
Best Local Similarity: 75.52%          Matches:       108
Query Match:           72.64%          Conservative:  13
DB:                    7.64e-57        Mismatches:    21
                                       Indels:        1
                                       Gaps:          0
```

```
Qy   1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer  20
         |||||||||:||||::|
Db 323 TGTGTGATTACTGCAAACCTACAGGCAAATACAAAAGGAATTTTCTGAGANTCCGGATAGT 382

Qy  21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln  40
         ||||||||||:||||||:::||
Db 383 GTNGCAAGCTGAAGATACAAANTATTGACATCAGANATTTNAGGACGACTGAGTCTTTGAAA 442

Qy  41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp  60
         ||::||||||||||:||||||:::|
Db 443 GACATAAAGTCTTTGGATACGGTGCTTCCTTCGTCATCTAGTCGAGATTCTATCTGGAC   502

Qy  61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgGlyIleSerSer-Le  80
         ||::||:
Db 503 AGGGTATTCAAAGTCTACCAGACCCCTGACCACCTACCCTGAGAAAGATCAGCAGCCCT   562

Qy  80 uAlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCy 100
         |||:::|||||
Db 563 CCCCAACTCCTTCTTCTTATCATCAAGAAGGACCTCCGAGTCTGTCANTCTCACATGGCATG 622

Qy 100 sHisCysGlyGluGluuAlaMetLysLysGlyTyrSerGlnIleIleLeuSerHisPheGluLysIle 120
         |||||||||||||:||
Db 623 TCATTGTGGGAGAAGCAANTGGAGAAAATACAACCAAAATTCTGAGTCACTTCATAGAGTT 682

Qy 120 uGluProGlnAlaAlaValValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMe 140
         ||::|
Db 683 GGAACTTCAGGCAGCGGTGGTAAAGGCTTCGGGGAGCAATTCTTCTGAGATGGAT     742

Qy 140 tGluGlu 142
         |||||||
Db 743 GGAGGAG 749
```

```
LOCUS       BB624019    676 bp    mRNA    linear    EST    26-OCT-2001
DEFINITION  BB624019 RIKEN full-length enriched, adult male eyeball Mus
            musculus cDNA clone 7530415H19 5', mRNA sequence.
ACCESSION   BB624019
VERSION     BB624019.1  GI:1646229
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 676)
AUTHORS     Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
            Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
            Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
            Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
            Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
TITLE       RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
JOURNAL     Unpublished (2001)
COMMENT     Contact: Yoshihide Hayashizaki
            RIKEN Genome Exploration Research Group, RIKEN Genomic
            Sciences Center (GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
            Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
            Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
            Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I.,
            Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
            Hayashizaki,Y.
            Computational Analysis of Full-length Mouse cDNAs Compared with
            Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
            RIKEN integrated sequence analysis (RISA) system-384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
            Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
            Sugahara,Y. and Hayashizaki,Y.
            Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
            Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
            and Hayashizaki,Y.
FEATURES           Location/Qualifiers
source             1..676
                   /organism="Mus musculus"
                   /mol_type="mRNA"
                   /strain="C57BL/6J"
                   /db_xref="taxon:10090"
                   /clone="7530415H19"
                   /sex="male"
                   /tissue_type="eyeball"
                   /dev_stage="adult"
                   /clone_lib="RIKEN full-length enriched, adult male
                   eyeball"
                   /lab_host="DH10B"
                   /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                   prepared and sequenced in Mouse Genome Encyclopedia
                   Project of Genome Exploration Research Group in Riken
                   Genomic Sciences Center and Genome Science Laboratory in
                   RIKEN. Division of Experimental Animal Research in Riken
                   contributed to prepare mouse tissues. 1st strand cDNA was
```

```
ORIGIN      primed with a primer [5'
            GAGAGAGAAGATCCAAGAGCTCTTTTTTTTTTTTTTTTTTVN 3'], cDNA was
            prepared by using trehalose thermo-activated reverse
            transcriptase and subsequently enriched for full-length by
            cap-trapper. cDNA went through one round of normalization
            to Rot = 10.0 and subtraction to Rot = 185.0. Second
            strand cDNA was prepared with the primer adapter of
            sequence [5' GAGAGAGATTCGCAGTTAATTAAATTAATCCCCCCCCCCC
            3']. cDNA was cloned into the XhoI and BamHI sites.
            Vector: a modified pBluescript KS(+) after bulk excision
            from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end:
            BamHI"
```

US-10-789-129-26 (1-144) x BB624019 (1-676)

Alignment Scores:
Pred. No.:
Score: 1.71e-46
                        461.00
Percent Similarity: 83.76%
Best Local Similarity: 74.36%
Query Match: 61.22%
DB: 2

```
Length:        676
Matches:        87
Conservative:   11
Mismatches:     19
Indels:          0
Gaps:            0
```

```
Qy    1 CysValIleAlaThrAsnLeuGlnGluIleArgArgAsnGlyPheSerAspIleArgGlySer  20
          ||||||||
Db  319 TGTGTGATTACTGCAAACCTACAGGCAATACAAAGGAATTTCTGAGAATTCGGATAGT      378

Qy   21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln     40
          :::||
Db  379 GTGCAAGCTGAAGATACAAATATTGACATCAGAATTTAAGGACGACACTGAGTCTTTGAAA   438

Qy   41 AspThrLysProAlaAsnArgCysSerLeuLeuArgHisLeuLeuTyrLeuAsp          60
          ||||||||
Db  439 GACATAAAGTCTTTGGATAGGTGCTGCTTCCTTCGTCATCTAGTGAGATTCTATCTGGAC   498

Qy   61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu     80
          ||||||
Db  499 AGGGTATTCAAAGTCTACCAGACCCCTGACCACCATACCCTGAGAAAGATCAGCAGCCTC   558

Qy   81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgCysHisIleAlaHisMetThrCys    100
          |||||||
Db  559 GCCAACTCCTTTCTTATCATCAAGAAGGACACCTCTGCGTCATTCTCACATGGCATGT     618

Qy  101 HisCysGlyGluGlyUalaMetLysLysSlysTyrSerGlnIleLeuSerHisPhe       117
          ||||||
Db  619 CATTGTGGGCGGGGAGGCANTGAGANATACAAACCAAAATTCTGAGTCACTTC          669
```

```
LOCUS       CR985515         647 bp    mRNA    linear     EST 28-JUN-2005
DEFINITION  CR985515 RZPD no. 9016 Homo sapiens cDNA clone RZPDp9016M1629 5',
            mRNA sequence.
ACCESSION   CR985515
VERSION     CR985515.1  GI:68279400
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 647)
  AUTHORS   Heil,O., Ebert,L., Hennig,S., Henze,S., Radelof,U., Schneider,D.
            and Korn,B.
  TITLE     Human T-Lymphocytes library
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Inge Arlart
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Heubnerweg 6, D-14059 Berlin, Germany
            Email: www.rzpd.de
            RZPD; RZPDp9016M1629.
            RZPDLIB; (Human T-Lymphocytes) RZPD LIB No.9016
            http://www.rzpd.de/cgi-bin/products/set.cgi?libNo=9016 Contact:
            Inge Arlart
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Heubnerweg 6, D-14059 Berlin, Germany
            Tel: +49 30 32639 100
            Fax: +49 30 32639 111
            www.rzpd.de
            This clone is available from RZPD;
            http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPDp9016M1629
            contact RZPD (product-support@rzpd.de) for further information.
            Primer name: qe3_4, Primer sequence: CGGATAACAATTCACACAG.
```

RESULT 6

CR985515

```
FEATURES            Location/Qualifiers
     source         1..647
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="RZPDp9016M1629"
                    /tissue_type="T-Lymphocytes"
                    /dev_stage="adult"
                    /lab_host="DH10B"
                    /clone_lib="RZPD no.9016"
                    /note="Vector: pQE80LSN_cloned; Site_1: SalI; Site_2:
                    NotI; vector:
                    http://www.rzpd.de/info/vectors/pQE80LSN_cloned_pic.shtml
                    ; 1st strand cDNA was prepared from mRNA obtained from
                    human T-Lymphocytes with a NotI - oligo(dT) primer [5'
                    GACTAGTTCTAGATCGCGAGCGGCCGCCCCTTTTTTTTTTTTTTTTT 3'].
                    Double-stranded cDNA was ligated to SalI adaptors,
                    digested with NotI and cloned into the NotI and SalI sites
                    of the pQE80LSN_cloned vector"
ORIGIN
```

US-10-789-129-26 (1-144) x CR985515 (1-647)

Alignment Scores:
Pred. No.:
Score: 5.58e-30
                        328.00
Percent Similarity: 66.20%
Best Local Similarity: 43.66%
Query Match: 43.56%
DB: 7

```
Length:        647
Matches:        62
Conservative:   32
Mismatches:     48
Indels:          0
Gaps:            0
```

```
Qy    1 CysValIleAlaThrAsnLeuGlnGluIleArgArgAsnGlyPheSerAspIleArgGlySer  20
          ||| :::||
Db  122 TGTCTGATTTCCACAGACATGCACCATATAGAAGAGGAGTTTCCAAGAAATCAAAAGAGCC  181

Qy   21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln     40
          ||| :::
Db  182 ATCCAAGCTAAGGACGACACCTTCCCAAAATGTCACTACCCTGTCCACATTGGAGACTGCAG  241

Qy   41 AspThrLysProAlaAsnArgCysSerLeuLeuArgHisLeuLeuTyrLeuAsp          60
          ||| :::
Db  242 ATCATTAAGCCCTTAGATGTGTTGCGGTGACCAAGAAACCTCCTGCGGTTCTACGTGGAC   301

Qy   61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu     80
          ||||| :::
Db  302 AGGGTGTTCAAAGGATCATCAGGAGCCAAACCCAAAATCTTGAGAAAATCAGCAGCATT    361

Qy   81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgCysHisIleAlaHisMetThrCys    100
          ||||| :::||
Db  362 GCCAACTCTTTCCTCTACATGCAGAAAAACTCTGCGGCAATGTCAGAACAGAGGCAGTGT   421

Qy  101 HisCysGlyGluGlyUalaMetLysLysSlysTyrSerGlnIleLeuSerHisPheGluLysLeu 120
          |||||                              ::::::::::::||||
Db  422 CACTGCAGGCAGGAAGCCACCAATGCCACCAGAGTCATCCAGAGAAATGATCAGCTG     481

Qy  121 GluProGlnAlaAlaValLysLeuAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet    140
          |||                ::::::                              ||| :::
Db  482 GAGGTCCACGCGCTGCCATTAAATCCCTGGGAGAGCTCGACCGCTGTTTCTTAGCCTGGATT  541

Qy  141 GluGlu 142
          |||
          :::
Db  542 AATAAG 547
```

```
RESULT 7
LOCUS       BB064801
BB064801
DEFINITION  BB064801 RIKEN full-length enriched, adult male eyeball Mus
            musculus cDNA clone 7S3041S H19 3', mRNA sequence.
ACCESSION   BB064801
VERSION     BB064801.2  GI:16259849
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 695)
AUTHORS     Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
            Hara,A., Hiramoto,K., Hori,P., Ishii,Y., Ito,M., Kawai,J.,
            Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
            Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,T.,
            Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
TITLE       RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
JOURNAL     Unpublished (2001)
COMMENT     On Jun 14, 2000 this sequence version replaced gi:8522215.
            Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center (GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
            Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res.  10 (10), 1617-1630 (2000)
            Watahiki,M., Yoneda,Y., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
            wagi,K., Fujiwake,S., Ishikawa,T., Ozawa,K., Tanaka,T.,
            Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
            and Hayashizaki,Y.
            RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
            Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
            Sugahara,Y. and Hayashizaki,Y.
            Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res.  11 (2), 281-289 (2001)
            Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I.,
            Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
            Hayashizaki,Y.
            Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
            Please visit our web site (http://genome.gsc.riken.go.jp/) for
            further details.
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
FEATURES             Location/Qualifiers
     source          1..695
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="7S3041S H19"
                     /sex="male"
                     /tissue_type="eyeball"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="RIKEN full-length enriched, adult male
                     eyeball"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. cDNA went through one round of normalization
                     to Rot = 10.0 and subtraction to Rot = 185.0. Second
                     strand cDNA was prepared with the primer adapter of
                     sequence [5' GAGAGAGAGATTCGAGTTAATTAAATTAAATTACCCCCCCCC
                     3']. cDNA was cloned into the XhoI and BamHI sites.
                     Vector: a modified pBluescript KS(+) after bulk excision
                     from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end:
                     BamHI"
ORIGIN

US-10-789-129-26 (1-144) x BB064801 (1-695)

Alignment Scores:
Pred. No. :
Score:                   328.00
Percent Similarity:      88.24%
Best Local Similarity:   80.00%
Query Match:             43.56%

                            6.17e-30    Length:          695
                                        Matches:          68
                                        Conservative:      7
                                        Mismatches:       10
                                        Indels:            1
                                        Gaps:              0

Qy      58 TyrLeuAspArgValPheIleLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIle 77
           ||||||||||||||||   |  ||||       ||  ||  |||   :|||||||||||||||
Db       3 TATCTGGACAGGGTATTCAAAGTCTACCAGACCCTGACCNCCATACCCTGAGAAAGATC 62

Qy      78 SerSerIleuAlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHis 97
           |||||||||||||||| || |||||||||||||| ||||||||||||||| :|||||||
Db      63 AGCAGCCTCGCCAAATCCTTTCTTATCATCAAGAAGGACCTTCTCAGTCTGTCATTCTCAC 122

Qy      98 MetThrCysHisCysSerGlyGluGlnLaAlaMetLysHisLysTyrSerGlnIleLeuSerHisIlePhe 117
           |||||||||||||||| ||||||||| |||||||||||||||||||||||  |||||||
Db     123 ATGGCATGTCA-TGTCGGGAAGAAGCAATCGAGAAATACAACCAAATTCGAGTCACATTC 181

Qy     118 GluLysLeuGluProGlnAlaAlaValValLysAlaLeuGlyGluLeuAspIleLeuLeu 137
           :|||||| |||||||| ||||||||||||||||||||||||||||||||||||
Db     182 ATAGAGTTGGAACTTCAGGCAGCCGGTGGTAAAGGCTTTGGGAGAACTAGGCATTCTTCTG 241

Qy     138 GlnTrpMetGluGlu 142
           :::||||||||||||
Db     242 AGATGGATGGAGGAG 256
```

```
RESULT 8
LOCUS       CR992594
CR992594
DEFINITION  CR992594 RZPD no.9016 Homo sapiens cDNA clone R2PDp9016C1545 5',
            mRNA sequence.
ACCESSION   CR992594
VERSION     CR992594.1  GI:68286479
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 699)
AUTHORS     Heil,O., Ebert,L., Hennig,S., Henze,S., Radelof,U., Schneider,D.
            and Korn,B.
TITLE       Human T-Lymphocytes library
JOURNAL     Unpublished (2005)
COMMENT     Contact: Inge Arlart
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Heubnerweg 6, D-14059 Berlin, Germany
            Email: www.rzpd.de
```

RZPD; R2PD90l6Cl545.
RZPDLIB; (Human T-Lymphocytes) RZPD LIB No. 9016
http://www.rzpd.de/cgi-bin/products/set.cgi?libNo=9016 Contact:
Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available from RZPD;
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPD90l6Cl545
contact RZPD (product-support@rzpd.de) for further information.
Primer name: qe3_4 , Primer sequence: CGGATAACAATTCACAG.

FEATURES
source
　　1..699
　　/organism="Homo sapiens"
　　/mol_type="mRNA"
　　/db_xref="taxon:9606"
　　/clone="RZPD90l6Cl545"
　　/tissue_type="T-Lymphocytes"
　　/dev_stage="adult"
　　/lab_host="DH10B"
　　/clone_lib="RZPD no.9016"
　　/note="vector: pQE80LSN_cloned; Site_1: SalI; Site_2:
　　NotI; vector:
　　http://www.rzpd.de/info/vectors/pQE80LSN_cloned_pic.shtml
　　; 1st strand cDNA was prepared from mRNA obtained from
　　human T-Lymphocytes with a NotI - oligo(dT) primer (5'
　　GACTAGTTCTAGATCGCGAGCGGCCGCCCTTTTTTTTTTTTTTTT 3').
　　Double-stranded cDNA was ligated to SalI adaptors,
　　digested with NotI and cloned into the NotI and SalI sites
　　of the pQE80LSN_cloned vector"

ORIGIN

US-10-789-129-26 (1-144) x CR992594 (1-699)

Alignment Scores:
Pred. No.:
Score:　　　　　　　　6.22e-30
Percent Similarity:　328.00
Best Local Similarity:　66.20%
Query Match:　　　　　43.66%
DB:　　　　　　　　　43.56%
　　　　　　　　　　　7

Length:　　699
Matches:　　62
Conservative:　32
Mismatches:　48
Indels:　　　0
Gaps:　　　0

```
Qy    1 CysValIleAlaThrAsnLeuGlnIleuIleArgAsnGlyPheSerAspIleArgGlySer  20
          ||:|:||||||:|:|  |||||:|||||||
Db  128 TGTCTGATTTCCACGACATGCACCATATAGAAGAGAGTTTCAAGAAATCAAAAGAGCC  187

Qy   21 ValGlnIleAlaLysAspGlyAsnIleAspIleLeuArgThrGluSerLeuGln  40
          ::|||||||||||:
Db  188 ATCCAAGTTAAGGACACACTTCCCAAAATGTCACTAATCCCTGTCCACATTGGAGACTCTGCAG  247

Qy   41 AspThrLysProAlaAsnArgCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp  60
          :::  ::||||||:    ::::|:||
Db  248 ATCATTAAGCCCTTAGATGTGTCGTGCTGACCAAGAACCTCCTGGCGTTCTACGTGGAC  307

Qy   61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgGlyLysIleSerSerLeu  80
          |||||||||| | ||||||
Db  308 AGGGTGTTCAAGGAATCATACCAGACCCCAAAACCTTGAGAAAAATCAGGATGTCAGG  367

Qy   81 AlaAsnSerPheLeuThrIleLysLysLysAspLeuArgLeuCysHisAlaHisMetThrCys  100
          |||||||| ||||
Db  368 GCCAACTCTTTCCTCTACATGCAGAAAACTCTGCGGCAATGTCAGGAACAGAGGCAGTGT  427

Qy  101 HisCysGlyGlyUAlaMetLysGlyTyrSerGlnIleIleLeuSerHisPheGluLysLeu  120
          |||  :::::::||:::
Db  428 CACTGCAGGCAGGAAGCCACCAGAGTCATCCATGACAACTATGATCAGCTG  487

Qy  121 GluProGlnAlaAlaValValLysAlaLeuGlyGluLeuLeuLeuGlnTrpMet  140
          ||||||||||    :::||||
Db  488 GAGGTCCAGGCTGCTGCCATTAAATCCCTGGGGGAGGAGCTCGACGTCTTTCTAGCCTGGATT  547

Qy  141 GluGlu 142
```

Db
RESULT 9
CA309757/c

LOCUS　　CA309757　　762 bp　　mRNA　　linear
DEFINITION　UI-H-FT1-bic-n-07-0-UI.s1 NCI_CGAP FT1 Homo sapiens cDNA clone
　　　　UI-H-FT1-bic-n-07-0-UI 3', mRNA sequence.
ACCESSION　CA309757
VERSION　　CA309757.1　GI:24472811
KEYWORDS　EST.
SOURCE　　Homo sapiens (human)
ORGANISM　Homo sapiens
　　Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
　　Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
　　Hominidae; Homo.
REFERENCE　1 (bases 1 to 762)
AUTHORS　　NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE　　National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
　　　　Tumor Gene Index
JOURNAL　Unpublished (1997)
COMMENT　Contact: Robert Strausberg, Ph.D.
　　Email: cgapbs-r@mail.nih.gov
　　Tissue Procurement: Dr. Gary W. Hunninghake, U of I
　　cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
　　cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
　　DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
　　Clone Distribution: Clone distribution information can be obtained
　　from Dr. M. Bento Soares, bento-soares@uiowa.edu
　　Seq primer: M13 FORWARD
　　POLYA=Yes.

FEATURES
source
　　1..762
　　/organism="Homo sapiens"
　　/mol_type="mRNA"
　　/db_xref="taxon:9606"
　　/clone="UI-H-FT1-bic-n-07-0-UI"
　　/tissue_type="Alveolar Macrophage"
　　/dev_stage="Adult"
　　/lab_host="DH10B (Life Technologies)"
　　/clone_lib="NCI_CGAP FT1"
　　/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
　　modified polylinker; Site_1: EcoR I; Site_2: Not I;
　　NCI_CGAP FT1 is a normalized cDNA library constructed from
　　a pool of 81 RNA samples from Alveolar Macrophages
　　challenged with different treatments. The mRNA samples
　　were a mixture of these conditions (times refer to
　　incubations following isolation by bronchoalveolar lavage)
　　(some normal donor macrophages were cultured in some of
　　the conditions, other donor macrophages in different
　　conditions). The mRNA samples were pooled for library
　　construction. Control 0 hours; control 3 hours; control 24
　　hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24
　　hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, Klebsiella
　　PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
　　moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus
　　moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral
　　vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector
　　(Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500,
　　3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS
　　3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3
　　hours; wt adenovirus + LPS 24 hours. The library was
　　normalized according to Bonaldo, Lennon and Soares, Genome
　　Research, 6:791-806, 1996. First strand cDNA synthesis was
　　primed with an oligo-dT primer containing a Not I site.
　　Double stranded cDNA was ligated to an EcoR I adaptor,
　　digested with Not I, and cloned directionally into
　　pT7T3-Pac vector. The oligonucleotide used to prime the
　　synthesis of first-strand cDNA contains a library tag
　　sequence that is located between the Not I site and the
　　(dT)18 tail. The sequence tag for this library is
　　GGCCATGCCG. The tissue was provided by Dr. Gary W.
　　Hunninghake of the University of Iowa.
　　TAG_TISSUE=Human Lung Alveolar Macrophage

Db　　548 AATAAG 553
　　:::

Left column

ORIGIN

TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCC"

Alignment Scores:
Pred. No.:   2.75e-23
Score: 275.00
Percent Similarity: 65.00%
Best Local Similarity: 45.00%
Query Match: 36.52%
DB:

Length: 762
Matches: 54
Conservative: 24
Mismatches: 42
Indels: 0
Gaps: 0

US-10-789-129-26 (1-144) x CA309757 (1-762)

```
Qy  23 AlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGlnAspThr 42
          ||||||||| :::
Db 762 GCTAAGGACACCTTCCCAAATGTCACTATCCTGTCCACATTGGAGACTNTGCAGATCATT 703

Qy  43 LysProAlaAsnArgCysCysGluLeuLeuArgHisLeuLeuLeuTyrLeuAspArgVal 62
           ||| ::|||
Db 702 AAGCCCTNAGATGTGTCTGCTGCGACCAACAACCTTCCTGGCGTTNACGTGGCAGACGGTG 643

Qy  63 PheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeuAlaAsn 82
          |||:::: |||    ||||||
Db 642 TTCAAGGATCATCAGGAGCCCAAAACCCCAAAATCTTGAGAAAAATCAGCAGCATTGCCAAC 583

Qy  83 SerPheLeuThrIleLeuLysLysAspLeuArgLeuCysHisAlaHisMetThrCysHisCys 102
          |||
Db 582 TCTTTCCTNTNACATCCAGAAAAACTCTGGCGCAATCGTCAGGAACACAGAGCAGTGTCACTGC 523

Qy 103 GlyGluGluAlaMetLysGlyTyrSerGlnIleLeuSerGlnHisPheGluLysLeuGluPro 122
          :::||||
Db 522 AGGCGAGGAAGCCACCAAATGCCACGAGTCATCCANGACTANTGACATCAGCTGGAGGTC 463

Qy 123 GlnAlaAlaValAlaLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMetGluGlu 142
          :::
Db 462 CACGCTGCTGCCCATTAAAATCCCTGGGAGAGAGCGCTCAGCTCGGCTCTTCAGCCTGGATTAATAAG 403
```

RESULT 10
BF738279/c

LOCUS   BF738279   564 bp   mRNA   linear   EST 10-JAN-2001
DEFINITION   PM4-KT0045-151200-006-g02 KT0045 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF738279
VERSION   BF738279.1 GI:12065059
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominidae; Homo.
REFERENCE   1 (bases 1 to 564)
AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
             Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
             Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
             Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
             O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
             Simpson,A.J.
TITLE   Shotgun sequencing of the human transcriptome with ORF expressed
             sequence tags
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED   10737800
COMMENT   Contact: Simpson A.J.G.
             Laboratory of Cancer Genetics
             Ludwig Institute for Cancer Research
             Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
             Brazil
             Tel: +55-11-2704922
             Fax: +55-11-2707001
             Email: asimpson@ludwig.org.br
             This sequence was derived from the FAPESP/LICR Human Cancer Genome
             Project. This entry can be seen in the following URL
             (http://www.ludwig.org.br/scripts/gethtml2.pl?ti=PM4&t2=PM4-KT0045-
             151200-006-g02&t3=2000-12-15&t4=1)

Right column

FEATURES   Location/Qualifiers
     source   1..564
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="KT0045"
                     /note="Organ: bladder tumor; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-Library was made by cloning products
                     derived from ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 - Ludwig Institute for Cancer Research)
                     profiles into the puc 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."

Seq primer: puc 18 forward
High quality sequence stop: 556.

ORIGIN

Alignment Scores:
Pred. No.:   3.18e-23
Score: 273.00
Percent Similarity: 100.00%
Best Local Similarity: 98.00%
Query Match: 36.25%
DB:

Length: 564
Matches: 51
Conservative: 1
Mismatches: 0
Indels: 0
Gaps: 0

US-10-789-129-26 (1-144) x BF738279 (1-564)

```
Qy  43 LysProAlaAsnArgCysCysGluLeuLeuArgHisLeuLeuLeuTyrLeuAspArgVal 62
          :::||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 509 CAGCCTGCGGAATCGATGCGTCGTGGGCCGCCATTTGCTAAGACTCTATCTGGACAGGGTA 450

Qy  63 PheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeuAlaAsn 82
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 449 TTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAGAGATCAGCAGCCTCGGCCAAT 390

Qy  83 SerPheLeuThrIleLeuLysLysAspLeuArgLeuCys 94
          ||||||||||||||||||||||||||||||||||||
Db 389 TCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTGT 354
```

RESULT 11
CA306526/c

LOCUS   CA306526   748 bp   mRNA   linear   EST 05-AUG-2004
DEFINITION   UI-H-FT1-bhw-m-10-0-UI.s1 NCI_CGAP_FT1 Homo sapiens cDNA clone
             UI-H-FT1-bhw-m-10-0-UI 3', mRNA sequence.
ACCESSION   CA306526
VERSION   CA306526.1 GI:24465979
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominidae; Homo.
REFERENCE   1 (bases 1 to 748)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
             Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
             Email: cgapbe-r@mail.nih.gov
             Tissue Procurement: Dr. Gary W. Hunninghake, U of I
             Tissue Preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be obtained
             from Dr. M. Bento Soares, bento-soares@uiowa.edu
             Seq primer: M13 FORWARD
             POLYA=Yes.

FEATURES   Location/Qualifiers
     source   1..748
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"

```
                              /clone="UI-H-FT1-bhw-m-10-0-UI"
                              /tissue_type="Alveolar Macrophage"
                              /dev_stage="adult"
                              /clone_lib="NCI_CGAP_FT1"
                              /lab_host="DH10B (Life Technologies)"
                              /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                              modified polylinker; Site_1: EcoR I; Site_2: Not I;
                              NCI_CGAP_FT1 is a normalized cDNA library constructed from
                              a pool of 81 RNA samples from Alveolar Macrophages
                              challenged with different treatments. The mRNA samples
                              were a mixture of these conditions (times refer to
                              incubations following isolation by bronchoalveolar lavage)
                              (some normal donor macrophages were cultured in some of
                              the conditions, other donor macrophages in different
                              conditions). The mRNA samples were pooled for library
                              construction. Control 0 hours; control 3 hours; control 24
                              hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
                              PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
                              moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus
                              moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral
                              vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector
                              (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500,
                              3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS
                              3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3
                              hours; wt adenovirus + LPS 24 hours. The library was
                              normalized according to Bonaldo, Lennon and Soares, Genome
                              Research, 6:791-806, 1996. First strand cDNA synthesis was
                              primed with an oligo-dT primer containing a Not I site.
                              Double stranded cDNA was ligated to an EcoR I adaptor,
                              digested with Not I, and cloned directionally into
                              pT7T3-Pac vector. The oligonucleotide used to prime the
                              synthesis of first-strand cDNA contains a library tag
                              sequence that is located between the Not I site and the
                              (dT)18 tail. The sequence tag for this library is
                              GGCCATGCCG. The tissue was provided by Dr. Gary W.
                              Hunninghake of the University of Iowa."
                              TAG_TISSUE=Human Lung Alveolar Macrophage
                              TAG_LIB=UI-H-FT1
                              TAG_SEQ=GGCCATGCCG"

ORIGIN

US-10-789-129-26 (1-144) x CA306526 (1-748)

Alignment Scores:
Pred. No.:                    1
Score:                        4.69e-22
Percent Similarity:           265.00
Best Local Similarity:        65.79%
Query Match:                  44.74%
DB:                           35.19%
                              6

                    29  AspIleArgIleLeuArgArgThrGluSerLeuGlnAspThrGlyAspProAlaAsnArgCys  48
                        ::::::    |||||:   :::||||||||||||::||||||||:::||::||||||::||
                   744  AATGTCACTATCCTGTCCACATTGGAGACTTCTGCAGATCATTAGCCCTTAGAGATGTGTGC  685

                    49  CysLeuLeuArgHisLeuLeuArgLeuTyrLeuAspArgValPheLysBAsnTyrGlnThr  68
                        ||||::    :::::::||||||||||::||||||:::  ::|||||||::|||:::|||
                   684  TGCCTGACCAAGAACCTCTGGCCGTTCACGTGGAGACAGGGTGTCAAAGGATCATCAGGAG  625

                    69  ProAspHisTyrThrLeuArgLysIleSerSerLeuAlaAsnSerPheLeuThrIleLys  88
                        ||||      ||||||     ::|||:::::::::||||||:::||||::||||||||
                    69  CCAAACCCCAAAAATCTTGAGAAAAATCAGGCAGATGCCAACCTCTTCCNTNTACGTACGG  565

                    89  LysAspLeuArgLeuCysHisAlaHisMetThrCysHisSCysGlyGluAlaMetLys  108
                        |||      ||:|||||::|||||::::|||||||||||||     :||||||||||
                   564  AAAACTCTCGCGCAATGTCAGGAACAGAGGACAGTGTCACTGCAGGCAGGAAGCCACCAAT  505

                   109  LysTyrSerGlnIleLeuSerHisPheGlyLysGluProGlnAlaAlaValValLys  128
                        ||||          |||        ::::::::::::||||||||      :::||||
                   504  GCCACCAGAGTCATCCATGACAACTAATCAGCTGGGAGGTCCACGCGTCGCCGCATTAAA  445

                   129  AlaLeuGlyGluLeuAspIleLeuGlnTrpMetGluGlu  142
                        ::::||||||||||||||||||||::::   :::    :::
```

ORIGIN

RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer (5'
GAGAGAGAGGAATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'), cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 20.0 and subtraction to Rot = 459.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGATTCTCGAGTTAATTAATTAATTAAATCCCCCCCCC
3'], cDNA was cleaved with XhoI and BamHI. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
FLC I."

US-10-789-129-26 (1-144) x BB639581 (1-709)

Alignment Scores:
Pred. No.:   1.3e-17
Score: 229.00   Length: 709
Percent Similarity: 63.30%   Matches: 46
Best Local Similarity: 42.08%   Conservative: 23
Query Match: 30.41%   Mismatches: 38
DB: 2   Indels: 2
                                  Gaps: 1

Qy   35 ArgThrGluSerLeuGlnAspThr------LysProAlaAsnArgCysCysLeuLeuArg 52
          ||||| ::||::|||||||||
Db   33 AGGACTCTGCCTGCGAGGAGACACCCAGGAGCCTGGAGAGATGTGTCCTGCATGACCAAC 92

Qy   53 HisLeuLeuArgLeuTyrLeuAspArgValPheLysAspAsnTyrGlnThrProAspHisTyr 72
          :::||||||||| |||||||||||| ::|||::||||||
Db   93 AACCTGCTGACATTCTTACAGAGACAGGGTGTTTCAGGACCCATCAGGAGAGAAGCCTTGAG 152

Qy   73 ThrLeuArgLysIleSerSerLeuAlaAsnSerPheLeuThrIleLysLysAspLeuArg 92
          ||:||:|||||||||||||||||||||||||||||
Db   153 GTCTTTAAGGAGAATCAGCAGCATTGCCAACTCTTTCCTCGGTCCAGAAATCTCTGGAG 212

Qy   93 LeuCysHisAlaHisMetThrCysHisCysGlyGlyGluGluArgAsnGlyPheSerGln 112
          ||| ::|||||||| |||||||
Db   213 CGATGTCAGGTGCCACAGACAATGTAACTGCAGTCAGGAAGGCCACCAATGCAACTAGGAATC 272

Qy   113 IleLeuSerHisPheGluLysGlyLeuProGlnAlaAlaValValLysAlaLeuArgLeuGlu 132
          ::||||||||||| ||||||||::::|||||||:::||
Db   273 ATCCATGACAACTACACAAATCAGCTGGAGGTCTCATCTGCTCCCTTAAGTCTCTAGGAGAA 332

Qy   133 LeuAspIleLeuLeuGlnInTrpMetGlu 141
          |||:|||||||||:|||
Db   333 CTGAACATACTTTTAGCCTGGATTGAC 359

RESULT 13
CK800046
LOCUS   CK800046   897 bp   mRNA   linear   EST 25-FEB-2004
DEFINITION   AGENCOURT_18791077 NICHD_XGC_Te2N Xenopus laevis cDNA
              IMAGE:7203819 5', mRNA sequence.
ACCESSION   CK800046
VERSION   CK800046.1 GI:42812042
KEYWORDS   EST.
SOURCE   Xenopus laevis (African clawed frog)
  ORGANISM   Xenopus laevis
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
              Xenopodinae; Xenopus; Xenopus.
REFERENCE   1 (bases 1 to 897)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
  COMMENT   Contact: Daniela S. Gerhard, Ph.D.
              Office of Cancer Genomics
              National Cancer Institute / NIH
              Bldg. 31 Rm10A07 Bethesda, MD 20892
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: Igor B. Dawid
              cDNA Library Preparation: Express Genomics

FEATURES   Location/Qualifiers
     source   1..897
                     /organism="Xenopus laevis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8355"
                     /clone="IMAGE:7203819"
                     /tissue_type="Pooled samples from 6 adult male testis"
                     /clone_lib="NICHD_XGC_Te2N"
                     /lab_host="DH10B TonA"
                     /note="Organ: testis; Vector: pExpress-1; Site_1: EcoRV;
                     Site_2: NotI; RNA obtained from 6 adult male testis. cDNA
                     was primed using oligo-dT primer.
                     5'-pGACTAGTTCTAGATCGGACGCGGGCCGCCCC(T)25-3' and cloned into
                     the EcoRV/NotI sites of pExpress-1. Size-selection >1kb
                     resulted in an average insert size of 1.15 kb. This
                     primary, microquantity library is normalized to Cot5
                     (non-normalized primary library is NICHD XGC Te2) and was
                     constructed by Express Genomics (Frederick, MD). Note:
                     this is an NIH_XGC library"

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM15082 row: e column: 01
High quality sequence stop: 750.

ORIGIN

US-10-789-129-26 (1-144) x CK800046 (1-897)

Alignment Scores:
Pred. No.:   2.1e-17
Score: 228.50   Length: 897
Percent Similarity: 57.75%   Matches: 42
Best Local Similarity: 29.58%   Conservative: 40
Query Match: 30.35%   Mismatches: 59
DB: 7   Indels: 1
                                  Gaps: 1

Qy   1 CysValIleAlaThrAsnLeuGlnGluIleLeuArgAsnGlyPheSerAspIleArgGlySer 20
          ||| ::::
Db   294 TGCCCTGTGCTTTGGATATCCAAGAGTTTAAAAAAATACCATGAGTCTCAAAGAGGTC 353

Qy   21 ValGlnAlaLysAspGlyAsnIleAspAspIleArgIleLeuArgArgThrGluSerLeuGln 40
          ::: |||||||||
Db   354 TTGCACAAAAAAGGATGTGATTACAGATGTCAGCCTCTG---AAAGCCCAAAAGTGCTGAAT 410

Qy   41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
          ||||| ::|:|||||||||
Db   411 CAGATACATCCATCCTGAGCAAATCTGCTTCCTTCTCAAAACTGGGGACGTTTTACATGAAC 470

Qy   61 ArgValPheLysAspAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
          :::::|||| :::
Db   471 AATATTTTCCCAAAACTGGAAAATCTCTTCAATTAGGACGACTTTAATCATTTA 530

Qy   81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
          :::||::||| |||||||
Db   531 GCTAACTCTGTCCTGGGTCTAAAGATAGAGCTCAAGCATTGTCATTCTTCTATGAGGTGT 590

Qy   101 HisCysGlyGlyGluGluArgAsnGlyPheSerGlnIleLeuSerHisPheGluLysGlyLeu 120
          |||||:::|||||||||||||
Db   591 CCCTGTGGGTGATCAGTCACACAAAATTATGGAAGACAGTTTAGGGAAGAAACCTTTACCAGG 650

Qy   121 GluProGlnAlaAlaValValLysAlaLeuArgLeuGluLeuAspIleLeuLeuGlnInTrpMet 140
          :::|||||||||:::|||||||
Db   651 GAGACAGAAGCAGCTATTATTAAAGCTATCGGAGACTTGAAATATCCTGATTCGCTGGTTG 710

Qy   141 GluGlu 142
          ||:|:
Db   711 GAAAAA 716

RESULT 14
CD366952/c
LOCUS   CD366952   658 bp   mRNA   linear   EST 05-AUG-2004

```
DEFINITION   UI-H-FT2-bjp-i-22-0-UI.s1 NCI_CGAP_FT2 Homo sapiens cDNA clone
             UI-H-FT2-bjp-i-22-0-UI 3', mRNA sequence.
ACCESSION    CD366952
VERSION      CD366952.1  GI:31151042
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominidae; Homo.
REFERENCE    1  (bases 1 to 658)
AUTHORS      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE        National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
             Tumor Gene Index
JOURNAL      Unpublished (1997)
COMMENT      Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Dr. Gary W. Hunninghake, U of I
             cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Distribution information can be found at
             http://genome.uiowa.edu/distribution/cgap.html
             POLYA=Yes.
             Seq primer: M13 FORWARD
FEATURES     Location/Qualifiers
     source  1..658
             /organism="Homo sapiens"
             /mol_type="mRNA"
             /db_xref="taxon:9606"
             /clone="UI-H-FT2-bjp-i-22-0-UI"
             /tissue_type="Alveolar Macrophage"
             /dev_stage="Adult"
             /clone_lib="NCI_CGAP_FT2"
             /lab_host="DH10B (Life Technologies)"
             /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
             modified polylinker; Site_1: EcoR I; Site_2: Not I;
             NCI_CGAP_FT2 is a subtracted cDNA library constructed from
             a pool of 81 RNA samples from Alveolar Macrophages
             challenged with different treatments. The mRNA samples
             were a mixture of these conditions (times refer to
             incubations following isolation by bronchoalveolar lavage)
             (some normal donor macrophages were cultured in some of
             the conditions, other donor macrophages in different
             conditions). The mRNA samples were pooled for library
             construction. Control 0 hours; control 3 hours; control 24
             hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
             PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
             moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph
             aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours;
             Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours;
             Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt
             adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24
             hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours;
             wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours.
             The library was subtracted according to Bonaldo, Lennon
             and Soares, Genome Research, 6:791-806, 1996. The tissue
             was provided by Dr. Gary W. Hunninghake of the University
             of Iowa.
ORIGIN
```

```
US-10-789-129-26 (1-144) x CD366952 (1-658)

Alignment Scores:
Pred. No.:
Score:              3.65e-16          Length:          658
Score:              217.00            Matches:         41
Percent Similarity: 68.24%            Conservative:    17
Best Local Similarity: 48.24%         Mismatches:      27
Query Match:        28.82%            Indels:          0
DB:                 6                 Gaps:            0
```

```
Qy  58 TyrLeuAspArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIle  77
        |||||||||||| |||||||| |||||||||| ||||| :::::: ||||||
Db 657 TACGTCGGACAGGGTGTTCAAGAATCATCAGGAGCCAAAACCCCAAAATCTTGAGAAAATC 598

Qy  78 SerSerLeuAlaAsnSerPheLeuThrIleLeuLysLysAspLeuArgLeuCysHisAlaHis  97
        |||||||| :::|||||| ::: |||||||||| ::: |||
Db 597 AGCAGCGATTGCGAACTCTTTCCTCTACATCGAGAAACTCTGCGGCCAATGTCAGGACAG 538

Qy  98 MetThrCysHisSerGlyGlyGluAlaMetLysLysTyrSerGlnIleIleLeuSerHisPhe 117
        ||||||||||| :::||| ||||| :::||||||
Db 537 AGGCAGTGTCACTCGACGAGGAGGAAGCCACCAATGCCACCAGAGTCATCCATGACAGTAT 478

Qy 118 GluLysLeuGluProGlnAlaAlaValValLysAlaLeuLeuGlyGluLeuAspIleLeuLeu 137
        ||||| |||||||||| |||||||||||||||||| :::
Db 477 GATCAGCTGAGGGTCCACGCTGCTCCCATTAAATCCCTGGAGAGACTCGAACGTCTTCTA 418

Qy 138 GlnTrpMetGluGlu 142
        ||| :::
Db 417 GCCTGGATTAATAAG 403
```

```
TAG TISSUE=Human Lung Alveolar Macrophage
TAG LIB=UI-H-FT2
TAG SEQ=GGCCATGCCG
```

```
RESULT 15
LOCUS        AW637118      538 bp    mRNA      linear    EST 26-APR-2001
DEFINITION   b154f02.w1 Blackshear/Soares normalized Xenopus egg library Xenopus
             laevis cDNA clone PBX0054F02 5', mRNA sequence.
ACCESSION    AW637118
VERSION      AW637118.1  GI:7394220
KEYWORDS     EST.
SOURCE       Xenopus laevis (African clawed frog)
ORGANISM     Xenopus laevis
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
             Xenopodinae; Xenopus; Xenopus.
REFERENCE    1  (bases 1 to 538)
AUTHORS      Blackshear,P.J., Lai,W.S., Thorn,J.M., Kennington,E.A., Staffa,N.G.,
             Jr., Moore,D.T., Bouffard,G.G., Beckstrom-Sternberg,S.M.,
             Touchman,J.W., Bonaldo,M.F. and Soares,M.B.
TITLE        The NIEHS Xenopus maternal EST project: interim analysis of the
             first 13,879 ESTs from unfertilized eggs
JOURNAL      Gene 267 (1), 71-87 (2001)
PUBMED       11311557
COMMENT      Contact: Perry J. Blackshear
             Office of Clinical Research and Laboratory of Signal Transduction
             National Institute of Environmental Health Sciences
             A2-05 NIEHS, 101 Alexander Drive, Research Triangle Park, NC 27709,
             USA
             Tel: 919 541-4899
             Fax: 919 541-4571
             Email: black009@niehs.nih.gov
             Clone is available through Research Genetics, Inc., 2130 Memorial
             Parkway, Huntsville, AL 35901
             phone 800-533-4363 ext.cdna, fax 256-536-9016 att:cdna, email
             cdna@resgen.com
             DNA Sequencing and analyses performed by National Institutes of
             Health Intramural Sequencing Center (NISC).
             PCR Primers
             FORWARD: TCTAAAAACGACGGCCAGT
             BACKWARD: CAGGAAACAGCTATGACC
             Plate: 0054 row: F column: 02
             Seq primer: T7 primer
FEATURES     Location/Qualifiers
     source  1..538
             /organism="Xenopus laevis"
             /mol_type="mRNA"
             /db_xref="taxon:8355"
             /clone="PBX0054F02"
             /sex="female"
             /tissue_type="unfertilized egg"
             /cell_type="unfertilized egg"
             /dev_stage="unfertilized egg"
             /lab_host="DH10B"
             /clone_lib="Blackshear/Soares normalized Xenopus egg
```

ORIGIN

```
                     library"
                     /note="vector: pT7T3-Pac; Site_1: EcoRI; Site_2: NotI;
                     PolyA-selected mRNA was prepared from unfertilized Xenopus
                     laevis eggs.  The library was constructed in the vector
                     pT7T3-Pac as described in Bonaldo, M.F., Lennon, G. and
                     Soares, M.B. 'Normalization and subtraction: two
                     approaches to facilitate gene discovery', Genome Research
                     6:791-806, 1996.  The first strand synthesis used a
                     NotI-dT18 primer; double stranded cDNAs were ligated to
                     EcoRI adapters, digested with NotI, and directionally
                     cloned into the NotI and EcoRI-digested pT7T3-Pac vector.
                     The library contained approximately 7.2 X 10^5
                     recombinants, with average insert sizes of 1-1.5 kb."
```

US-10-789-129-26 (1-144) x AW637118 (1-538)

Alignment Scores:

Pred. No.:	1
Score:	206.50
Percent Similarity:	59.66%
Best Local Similarity:	32.77%
Query Match:	27.42%
DB:	

Length:	538
Matches:	39
Conservative:	32
Mismatches:	47
Indels:	1
Gaps:	1

```
Qy    24 LysAspGlyAsnIleAspIleArgIleLeuArgThrGluSerLeuGlnAspThrLys 43
            |||||          |:::  ||| :    :::   ||  :::
Db    85 AAGGATGTGAATTACAGATGTCAGCCTCCTG---AAAGCCAAAGTGCTGAATCAGATACAT 141

Qy    44 ProAlaAsnArgCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAspArgValPhe 63
            |||:::||||||| ||:|| :|| |   ||:|||::|::::
Db   142 CCATCTGAGCAAATGCTGCTTCCTTCTCAAACTGGGACGTTTTTACATGAACAATATTTTC 201

Qy    64 LysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeuAlaAsnSer 83
                         :::            :::
Db   202 CCAAAACTGGAAATCTCTTCAAATTAAGGACCAGAAAGGTCTTAATCATTTAGCTAACTCT 261

Qy    84 PheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCysHisCysGly 103
            |||      |:||||  :::|||:|:    |||    ::  |||
Db   262 GTCCTGGGGTCTAAAGATAGAGCTCAAGCATTGTCATTCTTCTTCTATGAGGTGTCCCTGGT 321

Qy   104 GluGluAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeuGluProGln 123
            :::::::::||||||       |                 :::::::|||||   :::
Db   322 GATCAGTCACACAAAATTATGGAAAGACTTTAGGGAAAAACCTTTTACCAGATGAGACAGAA 381

Qy   124 AlaAlaLeuValLysAlaLeuGlyLeuAspIleLeuLeuGlnTrpMetGluGlu 142
            |||||||:|:::||||||:|:::|||||||||:|::|||||||:::|:::
Db   382 GCAGCTATTATTAAAGCTATTGGAGACTTGAATATCCTGATTCGCTGGGTTGGGAAAA 438
```

```
                                          GenCore version 5.1.6
                                    Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on:            December 28, 2005, 14:19:09 ; Search time 820 seconds
                                                 (without alignments)
                                                 1452.183 Million cell updates/sec

Title:             US-10-789-129-26
Perfect score:     753
Sequence:          1 CVIAYNLQEIRNGPSDIRGS.........AVVKALGELDILLQWMEETE 144

Scoring table:     BLOSUM62
                   Xgapop  10.0 ,  Xgapext  0.5
                   Ygapop  10.0 ,  Ygapext  0.5
                   Fgapop   6.0 ,  Fgapext  7.0
                   Delop    6.0 ,  Delext   7.0

Post-processing:   Minimum Match  0%
                   Maximum Match 100%
                   Listing first 45 summaries

Searched:          9793542 seqs, 413468905 residues

Total number of hits satisfying chosen parameters:    19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Command line parameters:
  -MODEL=frame+_p2n.model   -DEV=x1p
  -Q=/cgn2_1/USPTO_spool_p/US10789129/runat_23122005_152721_20318/app_query.fasta_1.327
  -DB=Published_Applications_NA_Main   -QFMT=fastap  -SUFFIX=p2n.rnpbm
  -MINMATCH=0.1  -LOOPCL=0   -UNITS=bits  -START=1  -END=-1
  -MATRIX=blosum62  -TRANS=human40.cdi  -LIST=45  -DOCALIGN=200  -THR_SCORE=pct
  -THR_MAX=100  -THR_MIN=0  -ALIGN=15  -MODE=LOCAL  -OUTFMT=pto  -NORM=ext
  -HEAPSIZE=500  -MINLEN=0  -MAXLEN=200000000000
  -USER=US10789129 @CGN_1_1 1549 @runat 23122005 152721 20318 -NCPU=6 -ICPU=3
  -NO_MMAP  -LARGEQUERY  -NEG_SCORES=0  -WAIT  -DSPBLOCK=100 -LONGLOG
  -DEV_TIMEOUT=120  -WARN_TIMEOUT=30  -THREADS=1  -XGAPOP=10  -XGAPEXT=0.5  -FGAPOP=6
  -FGAPEXT=7  -YGAPOP=10  -YGAPEXT=0.5  -DELOP=6  -DELEXT=7

Database :         Published_Applications_NA_Main:*
  1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
  2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
  3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
  4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
  5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
  6: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
  7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
  8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
  9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	753	100.0	926	6	US-10-321-163-1	Sequence 1, Appli
2	753	100.0	926	6	US-10-413-661-1	Sequence 1, Appli
3	753	100.0	926	6	US-10-172-118-186	Sequence 186, App
4	753	100.0	926	7	US-10-342-887-186	Sequence 186, App
5	753	100.0	926	7	US-10-789-129-1	Sequence 1, Appli
6	753	100.0	926	7	US-10-789-251-1	Sequence 1, Appli
7	753	100.0	926	7	US-10-789-968-1	Sequence 1, Appli

8	753	100.0	926	8	US-10-748-484-1	Sequence 1, Appli
9	753	100.0	926	8	US-10-994-116-1	Sequence 17, Appl
10	753	100.0	926	9	US-10-994-151-1	Sequence 1, Appli
11	749	99.5	926	6	US-10-122-882B-14	Sequence 14, Appl
12	749	99.5	462	8	US-10-122-882B-18	Sequence 18, Appl
13	749	99.5	462	6	US-11-054-063-18	Sequence 18, Appl
14	749	99.5	513	6	US-09-946-374-401	Sequence 401, App
15	746	99.1	867	7	US-10-807-837-7	Sequence 7, Appli
16	749	99.5	867	7	US-10-466-695A-1	Sequence 1, Appli
17	739	98.1	926	8	US-10-006-867-137	Sequence 137, App
18	739	98.1	1571	3	US-11-054-063-137	Sequence 137, App
19	739	98.1	1571	6	US-10-052-586-609	Sequence 609, App
20	739	98.1	1571	7	US-10-063-547-137	Sequence 137, App
21	739	98.1	1571	5	US-10-063-551-137	Sequence 137, App
22	739	98.1	1571	5	US-10-028-072-97	Sequence 97, Appl
23	739	98.1	1571	5	US-10-028-072-545	Sequence 545, App
24	739	98.1	1571	5	US-10-174-590-609	Sequence 609, App
25	739	98.1	1571	5	US-10-176-758-609	Sequence 609, App
26	739	98.1	1571	5	US-10-175-737-609	Sequence 609, App
27	739	98.1	1571	5	US-10-063-616-137	Sequence 137, App
28	739	98.1	1571	5	US-10-174-581-609	Sequence 609, App
29	739	98.1	1571	5	US-10-176-483-609	Sequence 609, App
30	739	98.1	1571	5	US-10-176-749-609	Sequence 609, App
31	739	98.1	1571	5	US-10-176-914-609	Sequence 609, App
32	739	98.1	1571	5	US-10-176-915-609	Sequence 609, App
33	739	98.1	1571	5	US-10-140-808-97	Sequence 97, Appl
34	739	98.1	1571	5	US-10-140-808-545	Sequence 545, App
35	739	98.1	1571	5	US-10-063-569-137	Sequence 137, App
36	739	98.1	1571	5	US-10-063-513-137	Sequence 137, App
37	739	98.1	1571	5	US-10-063-515-137	Sequence 137, App
38	739	98.1	1571	5	US-10-063-512-137	Sequence 137, App
39	739	98.1	1571	5	US-10-121-049-97	Sequence 97, Appl
40	739	98.1	1571	5	US-10-121-049-545	Sequence 545, App
41	739	98.1	1571	5	US-10-173-706-609	Sequence 609, App
42	739	98.1	1571	5	US-10-175-738-609	Sequence 609, App
43	739	98.1	1571	5	US-10-175-752-609	Sequence 609, App
44	739	98.1	1571	5	US-10-176-482-609	Sequence 609, App
45	739	98.1	1571	5	US-10-176-757-609	Sequence 609, App

ALIGNMENTS

```
RESULT 1
US-10-321-163-1

; Sequence 1, Application US/10321163
; Publication No. US20030161811A1
; GENERAL INFORMATION:
;  APPLICANT: Chandrasekher, Yasmin
;  APPLICANT: McKernan, Patricia
;  TITLE OF INVENTION: METHOD FOR TREATING CERVICAL CANCER
;  FILE REFERENCE: 01-44US
;  CURRENT APPLICATION NUMBER: US/10/321,163
;  CURRENT FILING DATE:  2002-12-17
;  PRIOR APPLICATION NUMBER: 60/341,783
;  PRIOR FILING DATE: 2001-12-17
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: FastSEQ for Windows Version 3.0
;
; SEQ ID NO 1
;  LENGTH: 926
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (45)...(572)
US-10-321-163-1

  Alignment Scores:
Pred. No.: 1
Score:                          8.29e-93
Percent Similarity:             753.00          Length:          926
Best Local Similarity:          100.00%         Matches:         144
Query Match:                    100.00%         Conservative:      0
DB:                                             Mismatches:        0
                                                Indels:            0
                                                Gaps:              0
```

US-10-789-129-26 (1-144) x US-10-321-163-1 (1-926)

```
Qy       1 CysValIleAlaThrAsnLeuGlnLeuIleArgAsnGlyPheSerAspIleArgGlySer 20
Db     141 TGTGTGATCGCTACAAACCTTCAGGAAATACGAAATGGATTTTCTGACATACGGGGGCAGT 200
```

```
Qy      21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
Db     201 GTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAA 260
```

```
Qy      41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
Db     261 GACACAAAAGCCTGCGAAATGGTGCCTCCTGCGCCATTTGCTAAGACTCTATCTGGAC 320
```

```
Qy      61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysLeuSerSerLeu 80
Db     321 AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGACTCAGCGCCTC 380
```

```
Qy      81 AlaAsnSerPheLeuThrIleLysGlyLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
Db     381 GCCAATTCCTTTCTTACCATCAAGAAGAGGACCTCCGGCTCTGTCATGCCCACATGACATGC 440
```

```
Qy     101 HisCysGlyGluGlyLeuAlaMetLeuLysGlyLysTyrSerGlnIleIleLeuSerHisPheGlyLysLeu 120
Db     441 CATTGTGGGGAGGGAAGCAATGAAGAAATACAGCCCAGATTCTGAGTCACTTTGAAAAAGCTG 500
```

```
Qy     121 GluProGlnAlaAlaValValLysLysAlaLeuGlyGluLeuAspIleLeuLeuLeuGlnTrpMet 140
Db     501 GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAAATGGGATG 560
```

```
Qy     141 GluGluThrGlu 144
Db     561 GAGGAGGACAGA 572
```

RESULT 2
US-10-413-661-1

; Sequence 1, Application US/10413661
; Publication No. US20030176657A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Haldeman, Betty A.
; TITLE OF INVENTION: MAMMALIAN CYTOKINE-LIKE POLYPEPTIDE-10
; FILE REFERENCE: 97-72
; CURRENT APPLICATION NUMBER: US/10/413,661
; CURRENT FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: 09/199,586
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/066,597
; PRIOR FILING DATE: 1997-11-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (45)...(572)

US-10-413-661-1

Alignment Scores:
Pred. No.:
Score: 8.29e-93
Percent Similarity: 753.00
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 6
                          Length: 926
                          Matches: 144
                          Conservative: 0
                          Mismatches: 0
                          Indels: 0
                          Gaps: 0

US-10-789-129-26 (1-144) x US-10-413-661-1 (1-926)

```
Qy       1 CysValIleAlaThrAsnLeuGlnLeuIleArgAsnGlyPheSerAspIleArgGlySer 20
Db     141 TGTGTGATCGCTACAAACCTTCAGGAAATACGAAATGGATTTTCTGACATACGGGGGCAGT 200
```

RESULT 3
US-10-172-118-186

; Sequence 186, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 186
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AF224266
; DATABASE ENTRY DATE: 2001-06-18

US-10-172-118-186

Alignment Scores:
Pred. No.:
Score: 8.29e-93
Percent Similarity: 753.00
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 6
                          Length: 926
                          Matches: 144
                          Conservative: 0
                          Mismatches: 0
                          Indels: 0
                          Gaps: 0

US-10-789-129-26 (1-144) x US-10-172-118-186 (1-926)

```
Qy       1 CysValIleAlaThrAsnLeuGlnLeuIleArgAsnGlyPheSerAspIleArgGlySer 20
Db     141 TGTGTGATCGCTACAAACCTTCAGGAAATACGAAATGGATTTTCTGACATACGGGGGCAGT 200
```

```
Qy   21  ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln   40
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  201  GTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGACGGAGTCTTTGCAA    260

Qy   41  AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuLeuTyrLeuAsp    60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  261  GACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTCTATCTGGAC  320

Qy   61  ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu  80
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  321  AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC  380

Qy   81  AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  381  GCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTGTCATGCCCACATGACATGC  440

Qy  101  HisCysGlyGluGluAlaMetLysLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  441  CATTGTGGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG 500

Qy  121  GluProGlnAlaAlaValValLysAlaLeuGlyLeuLeuAspIleLeuLeuGlnTrpMet 140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  501  GAACCTCAGGCAGCCAGTGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATG 560

Qy  141  GluGluThrGlu 144
         ||||||||||||
Db  561  GAGGAGACAGA  572
```

RESULT 4
US-10-342-887-186
; Sequence 186, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 186
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-186

Alignment Scores:
Pred. No.:
Score: 8.29e-93   Length: 926
Percent Similarity: 753.00   Matches: 144
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: Indels: 0
                                           Gaps: 0

US-10-789-129-26 (1-144) x US-10-342-887-186 (1-926)

```
Qy    1  CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer  20
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  141  TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGACATACGGGGCAGT 200

Qy   21  ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln  40
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  201  GTGCAAGCCAAAGATGGAAACATTGA  260
```

```
Qy   41  AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuLeuTyrLeuAsp    60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  261  GACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTCTATCTGGAC  320

Qy   61  ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu  80
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  321  AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC  380

Qy   81  AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  381  GCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTGTCATGCCCACATGACATGC  440

Qy  101  HisCysGlyGluGluAlaMetLysLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  441  CATTGTGGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG 500

Qy  121  GluProGlnAlaAlaValValLysAlaLeuGlyLeuLeuAspIleLeuLeuGlnTrpMet 140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  501  GAACCTCAGGCAGCCAGTGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATG 560

Qy  141  GluGluThrGlu 144
         ||||||||||||
Db  561  GAGGAGACAGA  572
```

RESULT 5
US-10-789-129-1
; Sequence 1, Application US/10789129
; Publication No. US20040142428A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Haldeman, Betty A.
; TITLE OF INVENTION: MAMMALIAN CYTOKINE-LIKE POLYPEPTIDE-10
; FILE REFERENCE: 97-72
; CURRENT APPLICATION NUMBER: US/10/789,129
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US/10/413,661
; PRIOR FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: 09/199,586
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/066,597
; PRIOR FILING DATE: 1997-11-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (45)...(572)
US-10-789-129-1

Alignment Scores:
Pred. No.:
Score: 8.29e-93   Length: 926
Percent Similarity: 753.00   Matches: 144
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: Indels: 0
                                           Gaps: 0

US-10-789-129-26 (1-144) x US-10-789-129-1 (1-926)

```
Qy    1  CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer  20
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  141  TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGACATACGGGGCAGT 200

Qy   21  ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln  40
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  201  GTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGACGGAGTCTTTGCAA  260
```

Left column

```
Qy   41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp  60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  261 GACACAAAGCCTGCGAATCGATCGGCCCATTGCTAAGACTCTATCTGGAC          320

Qy   61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu  80
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  321 AGGGTATTTAAAAACTACCAGACACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC 380

Qy   81 AlaAsnSerPheLeuThrIleLeuLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  381 GCCAATTCCTTTCTTACCATCAAGAAAGGACCTCCGGCTCTGTCAGCCCACATGACATGC  440

Qy  101 HisCysGlyGluGluAlaMetLysLysTyrSerGlnIleIleLeuSerHisHisPheGluLysLeu 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  441 CATTGTGGTGGAGGAAGCAATGAAGAAATACAGCCAGATTCTTGAAAAGCTG        500

Qy  121 GluProGlnAlaAlaValValLysAlaLeuLeuGlyLeuLeuAspIleLeuLeuGlnTrpMet 140
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  501 GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATG  560

Qy  141 GluGluThrGlu 144
        ||||||||||||
Db  561 GAGGAGACAGAA 572
```

RESULT 6
US-10-789-251-1

; Sequence 1, Application US/10789251
; Publication No. US20040143097A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Haldeman, Betty A.
; TITLE OF INVENTION: MAMMALIAN CYTOKINE-LIKE POLYPEPTIDE-10
; FILE REFERENCE: 97-72
; CURRENT APPLICATION NUMBER: US/10/789,251
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US/10/413,661
; PRIOR FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: 09/199,586
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/066,597
; PRIOR FILING DATE: 1997-11-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (45)...(572)
US-10-789-251-1

Alignment Scores:
Pred. No.:
Score: 8.29e-93   Length: 926
                       753.00   Matches: 144
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: 7   Gaps: 0

US-10-789-129-26 (1-144) x US-10-789-251-1 (1-926)

```
Qy    1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer  20
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  141 TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGACATACGGGGCCAGT 200

Qy   21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln  40
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  201 GTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAA  260

Qy   41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp  60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  261 GACACAAAGCCTGCGAATCGATCGGCCCATTGCTAAGACTCTATCTGGAC          320
```

Right column

```
Qy   61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu  80
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  321 AGGGTATTTAAAAACTACCAGACACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC 380

Qy   81 AlaAsnSerPheLeuThrIleLeuLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  381 GCCAATTCCTTTCTTACCATCAAGAAAGGACCTCCGGCTCTGTCAGCCCACATGACATGC  440

Qy  101 HisCysGlyGluGluAlaMetLysLysTyrSerGlnIleIleLeuSerHisHisPheGluLysLeu 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  441 CATTGTGGTGGAGGAAGCAATGAAGAAATACAGCCAGATTCTTGAAAAGCTG        500

Qy  121 GluProGlnAlaAlaValValLysAlaLeuLeuGlyLeuLeuAspIleLeuLeuGlnTrpMet 140
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  501 GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATG  560

Qy  141 GluGluThrGlu 144
        ||||||||||||
Db  561 GAGGAGACAGAA 572
```

RESULT 7
US-10-789-968-1

; Sequence 1, Application US/10789968
; Publication No. US20040152878A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Haldeman, Betty A.
; TITLE OF INVENTION: MAMMALIAN CYTOKINE-LIKE POLYPEPTIDE-10
; FILE REFERENCE: 97-72
; CURRENT APPLICATION NUMBER: US/10/789,968
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US/10/413,661
; PRIOR FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: 09/199,586
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/066,597
; PRIOR FILING DATE: 1997-11-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (45)...(572)
US-10-789-968-1

Alignment Scores:
Pred. No.:
Score: 8.29e-93   Length: 926
                       753.00   Matches: 144
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: 7   Gaps: 0

US-10-789-129-26 (1-144) x US-10-789-968-1 (1-926)

```
Qy    1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer  20
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  141 TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGACATACGGGGCCAGT 200

Qy   21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln  40
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  201 GTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAA  260

Qy   41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp  60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  261 GACACAAAGCCTGCGAATCGATCGGCCCATTGCTAAGACTCTATCTGGAC          320

Qy   61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu  80
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

Left column (RESULT 8)

```
Db    321 AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC 380
Qy     81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
Db    381 GCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTGTCAGCCCCACATGACATGC 440
Qy    101 HisCysGlyGluGluValaMetLysLysTyrSerGlnIleLeuSerHisPheGlyLysLeu 120
Db    441 CATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG 500
Qy    121 GluProGlnAlaAlaValaValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet 140
Db    501 GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATG 560
Qy    141 GluGluThrGlu 144
Db    561 GAGGAGACAGAA 572
```

RESULT 8
US-10-748-484-1

; Sequence 1, Application US/10748484
; Publication No. US20040181040A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Haldeman, Betty A.
; APPLICANT: Grossmann, Angelika
; TITLE OF INVENTION: MAMMALIAN CYTOKINE-LIKE POLYPEPTIDE-10
; FILE REFERENCE: 97-72
; CURRENT APPLICATION NUMBER: US/10/748,484
; CURRENT FILING DATE: 2003-12-29
; PRIOR APPLICATION NUMBER: US/09/199,586
; PRIOR FILING DATE: 1998-11-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (45)...(572)
US-10-748-484-1

Alignment Scores:
Pred. No.:
Score: 8.29e-93   Length: 926
Percent Similarity: 753.00   Matches: 144
Percent Local Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: 8   Gaps: 0

US-10-789-129-26 (1-144) x US-10-748-484-1 (1-926)

```
Qy      1 CysValIleAlaThrAsnLeuGlnGluIleGluArgAsnGlyPheSerArgAspIleArgGlySer 20
Db    141 TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGACATACGGGGCGAGT 200
Qy     21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
Db    201 GTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAA 260
Qy     41 AspThrArgLysProAlaAsnArgCysSerLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
Db    261 GACACAAAGCCTGCGAATCGATGCTCCCTGCTCCGGCACATTGCTAAGACTCTATCTGGAC 320
Qy     61 ArgValPheLysAsnTyrGlnThrProAspHisThrTyrThrLeuArgLysIleSerSerLeu 80
Db    321 AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC 380
Qy     81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
Db    381 GCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTGTCAGCCCCACATGACATGC 440
```

Right column (RESULT 9)

```
Qy    101 HisCysGlyGluGluValaMetLysLysTyrSerGlnIleLeuSerHisPheGlyLysLeu 120
Db    441 CATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG 500
Qy    121 GluProGlnAlaAlaValaValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet 140
Db    501 GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATG 560
Qy    141 GluGluThrGlu 144
Db    561 GAGGAGACAGAA 572
```

RESULT 9
US-10-994-116-1

; Sequence 1, Application US/10994116
; Publication No. US20050136004A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Wenfeng
; APPLICANT: Kindsvogel, Wayne
; APPLICANT: Chen, Zhi
; APPLICANT: Hughes, Steven D.
; APPLICANT: Chandrasekher, Yasmin A.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Lehner, Joyce M.
; APPLICANT: Siadak, Anthony W.
; APPLICANT: Sivakumar, Pallavur V.
; APPLICANT: Moore, Margaret D.
; TITLE OF INVENTION: ANTI-IL-20 ANTIBODIES AND BINDING PARTNERS AND METHODS OF USING
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 03-21
; CURRENT APPLICATION NUMBER: US/10/994,116
; CURRENT FILING DATE: 2004-11-19
; PRIOR APPLICATION NUMBER: US 60/524,131
; PRIOR FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/555,857
; PRIOR FILING DATE: 2004-03-24
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (45)...(575)
US-10-994-116-1

Alignment Scores:
Pred. No.:
Score: 8.29e-93   Length: 926
Percent Similarity: 753.00   Matches: 144
Percent Local Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: 9   Gaps: 0

US-10-789-129-26 (1-144) x US-10-994-116-1 (1-926)

```
Qy      1 CysValIleAlaThrAsnLeuGlnGluIleGluArgAsnGlyPheSerArgAspIleArgGlySer 20
Db    141 TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGACATACGGGGCGAGT 200
Qy     21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
Db    201 GTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAA 260
Qy     41 AspThrArgLysProAlaAsnArgCysSerLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
Db    261 GACACAAAGCCTGCGAATCGATGCTCCCTGCTCCGGCACATTGCTAAGACTCTATCTGGAC 320
Qy     61 ArgValPheLysAsnTyrGlnThrProAspHisThrTyrThrLeuArgLysIleSerSerLeu 80
Db    321 AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC 380
```

Left column

```
Qy  81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 381 GCCAATTCCTTCTTCTTACCATCAAGAAGGACCTCCGGCTCTGTCATGCCCACATGACATGC 440
Qy 101 HisCysGlyGluValAlaMetLysGlyTyrSerGlnIleIleLeuSerHisPheGluLysLeu 120
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 441 CATTGTGGGGAGGTAGCCATGAAGGGCTACTCTCAGATTATCCTGAGTCACTTTGAAAAGCTG 500
Qy 121 GluProGlnAlaAlaValValLysSerAlaLeuGlyIleLeuAspIleLeuLeuGlnMetTrpMet 140
       ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 501 GAACCTCAGGCAGCAGTTGTTAAGAGCGCTTTGGGGAACTAGACATTCTTCTGCAAATGGATG 560
Qy 141 GluGluThrGlu 144
       ||||||||||||
Db 561 GAGGAGACAGAA 572
```

RESULT 10
US-10-994-151-1
; Sequence 1, Application US/10994151
; Publication No. US20050170468A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Wenfeng
; APPLICANT: Kindsvogel, Wayne
; APPLICANT: Chen, Zhi
; APPLICANT: Hughes, Steven D.
; APPLICANT: Chandrasekher, Yasmin A.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Lehner, Joyce M.
; APPLICANT: Sladek, Anthony W.
; APPLICANT: Sivakumar, Pallavur V.
; APPLICANT: Moore, Margaret D.
; TITLE OF INVENTION: ANTI-IL-20 RECEPTOR ANTIBODIES AND BINDING PARTNERS AND METHODS O
; TITLE OF INVENTION: IN INFLAMMATION
; FILE REFERENCE: 04-17
; CURRENT APPLICATION NUMBER: US/10/994,151
; CURRENT FILING DATE: 2004-11-19
; PRIOR APPLICATION NUMBER: US 60/524,131
; PRIOR FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/555,857
; PRIOR FILING DATE: 2004-03-24
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (45)...(575)
; US-10-994-151-1

Alignment Scores:
Pred. No.:

Score:	8.29e-93
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	9

Length:	926
Matches:	144
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-10-789-129-26 (1-144) x US-10-994-151-1 (1-926)

```
Qy   1 CysValIleAlaThrAsnLeuGlnLeuIleArgAsnGlyPheSerAspIleArgGlySer 20
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 141 TGTGTGATCGCCACCAACCTTCAGGAAATACGGAACGGTTTCTCTGAGATCCGTGGCAGT 200
Qy  21 ValGlnAlaLysAspGlyAsnIleAspIleLeuArgAlaArgThrGluSerLeuGln 40
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 201 GTGCAAGCCAAAGATGGAAACATTGACATCAGAGGAGACTGAGTCTTTGCAA 260
Qy  41 AspThrLysProAlaAsnArgCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 261 GACACCAAAGCCTGCAAATCGANGCTGCCTCCGCCCATTTTGCTAAGACTCTATCTGGAC 320
```

Right column

```
Qy  61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgGlysIleSerSerLeu 80
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 321 AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC 380
Qy  81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 381 GCCAATTCCTTCTTCTTACCATCAAGAAGGACCTCCGGCTCTGTCATGCCCACATGACATGC 440
Qy 101 HisCysGlyGluValAlaMetLysGlyTyrSerGlnIleIleLeuSerHisPheGluLysLeu 120
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 441 CATTGTGGGGAGGTAGCCATGAAAGGCTACTCTCAGATTATCCTGAGTCACTTTGAAAAGCTG 500
Qy 121 GluProGlnAlaAlaValValLysSerAlaLeuGlyIleLeuAspIleLeuLeuGlnMetTrpMet 140
       ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 501 GAACCTCAGGCAGCAGTTGTTAAGAGCGCTTTGGGGGAACTAGACATTCTTCTGCAAATGGATG 560
Qy 141 GluGluThrGlu 144
       ||||||||||||
Db 561 GAGGAGACAGAA 572
```

RESULT 11
US-10-122-882B-14
; Sequence 14, Application US/10122882B
; Publication No. US20030228657A1
; GENERAL INFORMATION:
; APPLICANT: POWNDER, TRACEY
; APPLICANT: CHAN, CHUNG
; TITLE OF INVENTION: METHODS FOR ENHANCING THE TRANSLATION
; TITLE OF INVENTION: AND EXPRESSION OF RECOMBINANT PROTEINS
; FILE REFERENCE: 01-15
; CURRENT APPLICATION NUMBER: US/10/122,882B
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/283,668
; PRIOR FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: codon optimized for E. coli
; US-10-122-882B-14

Alignment Scores:
Pred. No.:

Score:	1.01e-92
Percent Similarity:	749.00
Best Local Similarity:	100.00%
Query Match:	99.31%
	99.47%
	6

Length:	462
Matches:	143
Conservative:	1
Mismatches:	0
Indels:	0
Gaps:	0

US-10-789-129-26 (1-144) x US-10-122-882B-14 (1-462)

```
Qy   1 CysValIleAlaThrAsnLeuGlnLeuIleArgAsnGlyPheSerAspIleArgGlySer 20
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  28 TGTGTGATCGCCACCAACCTGCAGCTGATCCGTAACGGTTTCTCTGAGATCCGTGGCAGC 87
Qy  21 ValGlnAlaLysAspGlyAsnIleAspIleLeuArgAlaArgThrGluSerLeuGln 40
       ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  88 GTGCAGGCCAAAGATGGTAACATTGACATCCTGCGTGCTCGTACCGAGTCTCTGCAG 147
Qy  41 AspThrLysProAlaAsnArgCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 148 GACACCAAAACCGGCGAACCGTTGCTGCGCCACCTGCTGCGTCTGTATCTGGAC 207
Qy  61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 208 CGTGTGTTTAAAAACTACCAGACCCCGGACCACTATACCCTGCGTAAAATCAGCAGCCTG 267
Qy  81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

RESULT 12

US-11-054-063-18

; Sequence 18, Application US/11054063
; Publication No. US20050164349A1
; GENERAL INFORMATION:
; APPLICANT: Chan, Chung
; APPLICANT: Powder, Tracey
; TITLE OF INVENTION: METHODS FOR ENHANCING EXPRESSION OF
; TITLE OF INVENTION: RECOMBINANT PROTEINS
; FILE REFERENCE: 03-22C1
; CURRENT APPLICATION NUMBER: US/11/054,063
; CURRENT FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: 11/008,853
; PRIOR FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: US 60/529,412
; PRIOR FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-054-063-18

Alignment Scores:
Pred. No.:   1.01e-92
Score: 749.00
Percent Similarity: 100.00%   Matches: 462
Best Local Similarity: 99.31%   Conservative: 1
Query Match: 99.47%   Mismatches: 0
DB: 10   Indels: 0
                                     Gaps: 0

US-10-789-129-26 (1-144) x US-11-054-063-18 (1-462)

Qy   1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
Db   1 TGTGTTGATCGCCACCAACCTGCAGGAAATCCGTAACGGTTTCTCTGAGATCCGTGGCAGC 60

Qy   21 ValGlnAlaLysAlaSerProGlyAsnIleLeuArgIleArgAsnGluArgGlnSerLeuGln 40
Db   61 ValGlnAlaLysAlaSerProGlyAsnIleLeuArgIleArgAsn 80

Qy   41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
Db   148 GACACCAAACCGGCAAACCGTTGCTGCCTGCTCGGCCACCTGCTGCGTCTGTATCTGGAC 207

Qy   61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgGlysIleSerSerLeu 80
Db   208 CGTGTTTTCAAAAACTACCAGACCCCGACCACTATACCCTGGTAAAATCAGCAGCCTG 267

Qy   81 AlaAsnSerPheLeuThrIleLeuLysLysAspLeuArgLeuCysHisSerAlaHisMetThrCys 100
Db   268 GCCAACTCCTTCCTGACCATCAAAAAAGACCTCCGTCTGTGCCACAGCGCCCATATGACTTGC 327

Qy   101 HisCysGlyGluGluIleAlaMetLysLysTyrSerGlnIleIleLeuSerHisPheGluLysLeu 120
Db   328 CACTGTGGTGAGGAAGCAATGAAAAAATACAGCCAGATTCTGCTCAGCCACTTCGAAAAACTG 387

Qy   121 GluProGlnAlaAlaValValLysAlaLeuGlyGluLeuAspIleIleLeuLeuGlnTrpMet 140
Db   388 GAACCGCAGGCAGCAGTGGTGAAAGCTCTGGGTGAACTGGACATTATCTGCTCCAGTGGATG 447

Qy   141 GluGluThrGlu 144
Db   448 GAGGAGACCGAA 459

RESULT 13

US-10-122-882B-17

; Sequence 17, Application US/10122882B
; Publication No. US20030228657A1
; GENERAL INFORMATION:
; APPLICANT: CHAN, CHUNG
; APPLICANT: POWNDER, TRACEY
; TITLE OF INVENTION: METHODS FOR ENHANCING THE TRANSLATION
; TITLE OF INVENTION: AND EXPRESSION OF RECOMBINANT PROTEINS
; FILE REFERENCE: 01-15
; CURRENT APPLICATION NUMBER: US/10/122,882B
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US/10/122,882B
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/283,668
; PRIOR FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 513
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion of EC and SEQ ID NO:14, codon optimized for
; OTHER INFORMATION: E. coli
US-10-122-882B-17

Alignment Scores:
Pred. No.:   1.19e-92
Score: 749.00
Percent Similarity: 100.00%   Matches: 143
Best Local Similarity: 99.31%   Conservative: 1
Query Match: 99.47%   Mismatches: 0
DB: 6   Indels: 0
                                     Gaps: 0

US-10-789-129-26 (1-144) x US-10-122-882B-17 (1-513)

Qy   1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
Db   1 TGTGTGATACGGCCACCAACCTGCAGGAAATCCGTAACGGTTTCTCTGAGATCCGTGGCAGC 138

Qy   21 ValGlnAlaLysAlaSerProGlyAsnIleLeuArgIleArgAsnGluArgGlnSerLeuGln 40
Db   139 GTGCAGGCGCCAAAGATGGTAACATTGACATCCGTAATCCCGCGTCCGAGTCTCTGCAG 198

Qy   41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
Db   199 GACACCAAACCGGCGAACCGTTGCTGCCTGCTCCGTCACCTGCTGCGTCTGTATCTGGAC 258

Qy   61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgGlysIleSerSerLeu 80
Db   259 CGTGTTTTCAAAAACTACCAGACCCCGACCACTATACCCTGGTAAAATCAGCAGCCTG 318

Qy   81 AlaAsnSerPheLeuThrIleLeuLysLysAspLeuArgLeuCysHisSerAlaHisMetThrCys 100
Db   319 GCCAACTCCTTCCTGACCATCAAAAAAGACCTCCGTCTGTGCCACAGCGCCCATATGACCTGC 378

Qy   101 HisCysGlyGluGluIleAlaMetLysLysTyrSerGlnIleIleLeuSerHisPheGluLysLeu 120
Db   379 CACTGTGGTGAGGAAGCAATGAAAAAATACAGCCAGATTCTGCTCAGCCACTTCGAAAAACTG 438

Qy   121 GluProGlnAlaAlaValValLysAlaLeuGlyGluLeuAspIleIleLeuLeuGlnTrpMet 140
Db   439 GAACCGCAGGCAGCAGTGGTGAAAGCTCTGGGTGAACTGGACATTATCTGCTCCAGTGGATG 498

Qy   141 GluGluThrGlu 144
Db   141 GAGGAGACCGAA 459

Db   499 GAGGAGACCGAA 510

RESULT 14
US-10-467-431-1
; Sequence 1, Application US/10467431
; Publication No. US20040092445A1
; GENERAL INFORMATION:
; APPLICANT: Heuer, Josef
; APPLICANT: Liu, Ling
; APPLICANT: Timothy, Noblitt
; FILE REFERENCE: X-14753
; TITLE OF INVENTION: USE OF LP82 TO TREAT HEMATOPOIETIC DISORDERS
; CURRENT APPLICATION NUMBER: US/10/467,431
; CURRENT FILING DATE: 2003-08-06
; PRIOR APPLICATION NUMBER: 60/272,242
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/332,740
; PRIOR FILING DATE: 2001-11-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin version 3.1
;
; SEQ ID NO 1
; LENGTH: 867
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (272)..(799)
; FEATURE:
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (272)..(325)
; OTHER INFORMATION:
US-10-467-431-1

Alignment Scores:
Pred. No.:
Score: 2.66e-92   Length: 867
                         749.00   Matches: 143
Percent Similarity: 100.00%   Conservative: 1
Best Local Similarity: 99.31%   Mismatches: 0
Query Match: 99.47%   Indels: 0
DB: 7   Gaps: 0

US-10-789-129-26 (1-144) x US-10-467-431-1 (1-867)

Qy   1 CysValIleAlaThrAsnLeuGlnGlnIleArgAsnGlyPheSerAspIleArgGlySer 20
         |||||||||||||||||||||||||||||||||||||||| |||:::||||||||||
Db 368 TGTGTGATCGCCACAAACCTTCAGGAAAATACGAAAATGGATTTTCTGAGATACGGGCAGT 427

Qy   21 ValGlnAlaLysAspGlyAsnIleAlaGlyIleArgIleLeuLeuArgAspGlySerLeuGln 40
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 428 GTGCAAGCCAAAGATGGAAACATTGCAGGAATCAGAATACTTAAGGAGGACTGAGTCTTTGCAA 487

Qy   41 AspThrLysProAlaLeuAsnArgCysTyrCysSerLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 488 GACACAAAAGCCTGCAAATCGATGCTCCTCCGCGGCGAAATCTTAAGACTTCTAAGACTTATACTGGAC 547

Qy   61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 548 AGGGTATTTAAAAACTACCAGACACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCCTC 607

Qy   81 AlaAsnSerPheLeuThrIleLysGlyAspLeuValArgLeuCysHisSerAlaHisSerMetThrCys 100
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db 608 GCCAATTCCTTTCTTACCATCAAGGGAGACCTCGTGCGTCTATGCCACATGACATGC 667

Qy 101 HisCysGlyGlyLeuAlaMetLysGlyLysTyrSerGlnIleLeuSerHisPheGluLysLeu 120
         |||||||||||||||||||||||||||||||||||||||||||||||
Db 668 CATTGTGGGGGAGGAGCCAATGAAGAAAATACAGCCAGAGTTCTGAGTCACTTTGAAAAGCTG 727

Qy 121 GluProGlnAlaLysAlaValValLysAlaLeuGlyLeuLeuAspIleLeuLeuGlnTrpMet 140
         ||||||||||||||||||||||||||||||||||||||||||||
Db 728 GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATG 787

Qy 141 GluGluThrGlu 144
         ||||||||||||
Db 788 GAGGAGACAGAA 799

Db 788 GAGGAGACAGAA 799
         |||||||||||
         GAGGAGACAGAA

RESULT 15
US-10-466-695A-1
; Sequence 1, Application US/10466695A
; Publication No. US20040162237A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Nyles W
; FILE REFERENCE: X-14544
; TITLE OF INVENTION: USE OF LP82 TO TREAT BODY WEIGHT DISORDERS
; CURRENT APPLICATION NUMBER: US/10/466,695A
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: 60/264,239
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin version 3.2
;
; SEQ ID NO 1
; LENGTH: 867
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (272)..(799)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (272)..(325)
US-10-466-695A-1

Alignment Scores:
Pred. No.:
Score: 2.66e-92   Length: 867
                         749.00   Matches: 143
Percent Similarity: 100.00%   Conservative: 1
Best Local Similarity: 99.31%   Mismatches: 0
Query Match: 99.47%   Indels: 0
DB: 7   Gaps: 0

US-10-789-129-26 (1-144) x US-10-466-695A-1 (1-867)

Qy   1 CysValIleAlaThrAsnLeuGlnGlnIleArgAsnGlyPheSerAspIleArgGlySer 20
         |||||||||||||||||||||||||||||||||||||||| |||:::||||||||||
Db 368 TGTGTGATCGCCACAAACCTTCAGGAAAATACGAAAATGGATTTTCTGAGATACGGGCAGT 427

Qy   21 ValGlnAlaLysAspGlyAsnIleAlaGlyIleArgIleLeuLeuArgAspGlySerLeuGln 40
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 428 GTGCAAGCCAAAGATGGAAACATTGCAGGAATCAGAATACTTAAGGAGGACTGAGTCTTTGCAA 487

Qy   41 AspThrLysProAlaLeuAsnArgCysTyrCysSerLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 488 GACACAAAAGCCTGCAAATCGATGCTCCTCCGCGGCGAAATCTTAAGACTTCTAAGACTTATACTGGAC 547

Qy   61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 548 AGGGTATTTAAAAACTACCAGACACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCCTC 607

Qy   81 AlaAsnSerPheLeuThrIleLysGlyAspLeuValArgLeuCysHisSerAlaHisSerMetThrCys 100
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db 608 GCCAATTCCTTTCTTACCATCAAGGGAGACCTCGTGCGTCTATGCCACATGACATGC 667

Qy 101 HisCysGlyGlyLeuAlaMetLysGlyLysTyrSerGlnIleLeuSerHisPheGluLysLeu 120
         |||||||||||||||||||||||||||||||||||||||||||||||
Db 668 CATTGTGGGGGAGGAGCCAATGAAGAAAATACAGCCAGAGTTCTGAGTCACTTTGAAAAGCTG 727

Qy 121 GluProGlnAlaLysAlaValValLysAlaLeuGlyLeuLeuAspIleLeuLeuGlnTrpMet 140
         ||||||||||||||||||||||||||||||||||||||||||||
Db 728 GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATG 787

Qy 141 GluGluThrGlu 144
         ||||||||||||
Db 788 GAGGAGACAGAA 799

Search completed: December 28, 2005, 16:28:55

This Page Blank (uspto)